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## ALIGNMENTS

BASE COUNT ORIGIN	FEATURES source	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION	DEFINITION	LOCUS	I32406	RESULT 1
/organism="unknown" 175 a 182 c 190 g 164 t	Location/Qualifiers 1. 711	diagnostic uses thereof Patent: US 5587458-A 1 24-DEC-1996;	Anti-erbB-2 antibodies, combinations thereof, and therapeutic and	King, C. Richter, Kasprzyk, P.G. and Bird, R.E.	1 (bases 1 to 711)	Unclassified.	Unknown.	Unknown.	-	g1823197	I32406	Sequence 1 from patent US 5587458.	132406 711 bp DNA PAT		
			and therapeutic and										07-JAN-1997		

Query Match

98.3%; Score 699.6; DB 6; Length 711;

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                      L (Dases 1 to 711)
Batra, J.K., Kasprzyk, P.G., B
Recombinant anti-erbB2 immunn
Proc. Natl. Acad. Sci. U.S.A.
92335198
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GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 108547] from the original journal article. This sequence comes from Fig. 1.
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JP 1997220092-A/2.
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Ekida, T., Yasukawa, K., Imanaka, T. and Takagi, M.

PRODUCTION OF SINGLE-STRAND FV ANTIBODY

Patent: JP 1997220092-A 2 26-AUG-1997;
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76; Conservative
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JP 1997220092-A/2
26-AUG-1997
15-FEB-1996 JP 1996027622
EKIDA TEIJI, YASUKAWA KIYOSHI, IMANAKA TADAYUKI,
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topology: Linear;
hypothetical: No;
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/db_xref="taxon:32644"
193 c 190 g 16
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Shimamura,T., Hamuro,J., Nakazawa,H., Ka
Shimamura,T., Hamuro,J., Nakazawa,H., Ka
Shimamura,T., Hamuro,J., Nakazawa,H., Ka
Takeshita,T.
Monoclonal antibodies which bind the gan
interleukin-2 receptor
Interleukin-2 receptor
Patent: US 5582826-A 1 10-DEC-1996;
Location/Qualifiers
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                         CGGAGGGGGGTCCAAGCTGGAAATAAAAGGTTCTA---CCTCTGGTTCTGGTAAATCTTC
                                                  CCCTGCTCCACTCAGTGGCGGTGGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGT
                                                                                                                                                               GAAGCCAGGATCCTCCCCCAAACTCTGGATTTATAGCACATCCAACCTGGCTTCTGGAGT
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Sequence 1 from patent US 5582826.
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Shimamura T., Hamuro J., Nakazawa H.
Shimamura T., Hamuro J., Nakazawa H.
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T "IMMUNOSUPPRESSIVE AGENT";
T "IMMUNOSUPPRESSIVE AGENT";
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Eukaryota;
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                                                 Mus sp. (mouse)
JP 1995313188-A/1
05-DEC-1995
21-APR-1994 JP 1994082836
21-APR-1994 JP 93P 94498
21-APR-1993 JP 93P 94491, 07-MAR-1994 JP 94P 36065
SHIMAMURA TOSHIAKI, HAMURO JUNJI, NAKAZAWA HARUMI,
KANAYAWA YUKA,
SUGAMURA KAZUO, TAKESHITA TOSHIICHI
C12P21/08,AG1K39/395,AG1K39/395,C12N1/21,C12N5/20,
C12N15/13/C12N15/06,
C12P21/08,C12R1:19),(C12P21/08,C12R1:91),(C12N1/21,C12R1:19);
strandedness: Double;
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/cell_type="hybridoma"
/cell_line="GP-2"
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/product="anti-IL-2 rece
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Pred. No. 2.2e-123;
1; Mismatches 136;
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                                         AAGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATGGAG
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King, C. Richter, Kasprzyk, P.G. and B
Anti-erbB-2 antibodies, combination:
diagnostic uses thereof
Patent: US 5587458-A 2 24-DEC-1996;
Location/Qualifiers
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DEFINITION ACCESSION
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 GTCTATTACTGTGCAAG------
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Ledbetter, J.A.,
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I45604
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Expression vectors encoding bispecific fusion proteins and of producing biologically active bispecific fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: US 5637481-A 29 10-JUN-1997;
Location/Qualifiers
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I31036
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Shimamura,T., Hamuro,J., Nakazawa,H., Kanayama,Y., Sugamura,K.
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Query Match
Best Local Similarity
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48.9%; milarity 71.5%; Conservative

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Patent number JP 1995313188-A/2, 05-DEC-1995
AJINOMOTO CO INC, SUGAMURA KAZUO,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimamura T., Hamuro J., Takeshita T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
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08-OCT-1997
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C12P21/08,A61K39/395,A61K39/395,C12N1/21,C12N5/20
C12N15/13//C12N15/06,
                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-1994 JP 1994082836
21-APR-1993 JP 93P 94491, 07-MAR-1994 JP 94P
SHIMANURA TOSHIAKI, HAMURO JUNJI, NAKAZAWA HARUMI
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                                    Artificial gene cDNA to mRNA.

artificial sequence
artificial sequence.

1 (bases 1 to 744)
Lee,T.K., Rollence,M.L., Hallberg,P.L., Oelkuct,M.
Nagle,J.W. and Filpula,D.R.
Production of engineered IgM-binding single-chain
                                                                                                                                                SYNDA44X 744 bp mRNA 9196 SYNDA44X 01-MAR-1996 Synthetic single-chain Fv fusion protein (DA4.4/212) mRNA, constructed from variable light and heavy chain regions of mouse monoclonal antibody DA4.4, 3' end of cds.
                                                                                                            monoclonal
                                                                                                                               g310739
                            Escherichia coli
                                                                                                                    igM-binding protein; fusion protein;
                                                                                                                                                                                                                                                    711
                   Microbiol.
 Location/Qualifiers
                                                                                                            antibody
                                                                                                                                                                                                                                                                                            -GTTACGGACTGGTACTTCGATGTCTGGGGCGCAGGGACCACGGTCAC
                   14
                   (5),
                    371-376
                                                                                                                     fusion
                                                                                                                     protein
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                                       antibodies
                                                                                                                      DA4.4/212;
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Query Match 47.5
Best Local Similarity 72.6
Matches 450; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 TATTTGGCCTGGTACCAGCAGAAACCAGGACAGTCTCCTGAACTTCTGGTATACTTTGCA 171
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                                                                   ACTGTAGACAAGTCGTCCAGCACAGCCTACATGGAGCTCCTCAGTCTGACATCTGAGGAC
                                                                                                                                          ATTGATCCTTACGATAGTGAAACTCTCTACAATCAAAGTTCAAGGACAAGGCCACACTG
                                                                                                                                                               ATTAATCCTTACAATGGTGATACTAACTACAACCAGAAGTTCAAGGGCAAGGCCACATTT
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TCTGCGGTCTATTACTGTGCAAGGGAAACTTATGATTACCCCCTTTGCTTACTGGGGCCAA
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382. .744
382. .744
/note="variable heavy chain antibody DA4.4 (ATCC HB57)"
a 187 c 186 g 179 t
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/product="fision protein"
/product="fision protein"
/db_xref="plD:9310740"
/translation="DVVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSNQKNYLAWYQQ
/translation="DVVMTQSPSSLAMSVGQKVTMSCKSSQSLLNSSNQKNYLAWYQQ
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TFGSGTKLEIKGSTSGSGKSSEGKGQVQLQQPGAEFVKPGAPVKLSCKASGYPFTTYW
VNMMKQNFGRGLEWIGRLDFYDSETLYNQKFKDKATLFVDKSSSTAYIQLSSLTSEDS
AVYYCARETYDYFFAYWGQGTLYTVS"
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/db_xref="taxon:29278"
<1. .735
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Pred. No. 9.2e-94;
1; Mismatches 166;
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GGGACTCTGGTCACTGTGTC

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BASE COUNT
ORIGIN
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SOURCE
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MEDLINE
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Best Local Similarity
Matches 479; Conser
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     CGACGATGTGCAGCTGGTGGAGTCTGGGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCCGGCA
                              TAAAGGTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGAAGCCTGGAGGTTCAATGAA
                                                                                   GGGGTCCAAGCTGGAAATAAAA----GGTTCTACCTCTGGTTCTGGAAATCTTCTGAAGG
                                                                                                                                        AGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGC
                                                                                                                                                                                                                                                                                            CACCATGACCTGCAGTGCCATCTCAACTGTAAGTTACATGCACTGGTACCAGCAGAGAGTC
                                                                                                                                                                                                                                                                                                                                               TCGCTTCAGTGGCAGTGGGTCTGGAAACTCTTACTCTCTCACGATCAGCAGCATGGAGGC
                                                                                                                                                                                               TCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGC
                                                                                                                                                                                                                                                                                                                    CACAATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCC 120
                                                                   GGGGACCAAGCTGGAGCTCAAAGAGGGTAAATCCTCAGGATCTGGCTCCGAATCCAAAGT
                                                                                                                         TGAAGATGTTGCCACTTATTACTGTTTTCAGGGGAGTGGGTACCCCGTACACGTTCGGAGG
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Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse hybridoma, CDNA to mRNA, and E.coli vector DNA.
artificial sequence
artificial sequence.
1 (bases 1 to 738)
Chaudhary, V.K., Batra, J.K., Gallo, M.G., Willingham, M.C.,
Fitzgerald, D.J. and Pastan, I.
A rapid method of cloning functional variable-region antibody in Escherichia coli as single-chain immunotoxins
Proc. Natl. Acad. Sci. U.S.A. 87, 1066-1070 (1990)
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C-region.
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326...365
/note="linker DNA"
193 c 192 g
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QAPEKGLEWVAYISRGGNTIYYANTVKGRFTISRDNPKNTLFLQMTSLRSDDTAMYYC
ARSHYYGYFYAMDYWGQGTTLTVSSKAF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="artificial:
/db_xref="taxon:29278"
<1. .>738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="OVB3 Ig light and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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AUTHORS
TITLE
JOURNAL
FEATURES
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Best Local S
Matches 447
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           GGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGACTT
                                                                   GTGGTGAAGCCTGGAGGTTCAATGAAGATATCCTGCAAGACTTCTGGTTACTCATTCACT
                                                                                                                         GGTTCTGGTAAATCTTCTGAAGGTAAAGGT---GTGCAGCTGCAGGAGTCAGGACCTGAG
                                                                                                                                                                                                                                      TCTCTCACAGTCAGGAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGG
                                                                                                                                                                                                                                                                            TCCGCTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTC
                                                                                                                                                                                                                                                                                             TCCAACCTKGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTAC
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GACCATGCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGGATAT
                                                     TTGGTGAAACCTGGGGCTTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTACACCTTCACT
                                                                                                            GGTAGCGGCAAATCCTCTGAAGGCAAAGGTCAGGTTCAGCTGCAGCAGTCTGACGCTGAG
                                                                                                                                                                 TATAGCTATCCCCTCACGTTCGGTGCTGGGACCAAGCTTGTGCTGAAAGGCTCTACTTCC
                                                                                                                                                                                  AGTCGTAGCCCACCCACCGTTCCGGAGGGGGGGTCCAAGCTGGAAATAAAAGGTTCTACCTCT
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Sequence
AR012822
g3971140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown.
Unclassified
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JS 5763733.
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TITLE
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Best Local Similarity
Matches 416; Conserv
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                                    GACCATGCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGGATAT
                                                    GGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTT
                                                                                                                                                      GGTTCTGGTAAATCTTCTGAAGGTAAAGGT----GTGCAGCTGCAGGAGTCAGGACCTGAG
                                                                                                                                                                                                      AGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAATAAAAGGTTCTACCTCT
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                                                                                                 GTGGTGAAGCCTGGAGGTTCAATGAAGATATCCTGCAAGACTTCTGGTTACTCATTCACT
                                                                                                                                                                                         TATAGCTATCCCCTCACGTTCGGTGCTGGGACCAAGCTTGTGCTGAAAGGCTCTACTTCC
                                                                                                                                                                                                                                          ACTOTOTOCATCAGCAGTGTGAAGACTGAAGACCTGGCAGTTTATTACTGTCAGCAGTAT 360
             ATTAATCCTTACAATGGTGATACTAACTACAACCAGAAGTTCAAGGGCAAGGCCACATTT
                                                                                                                                         GGTAGCGGCAAATCCTCTGAAGGCAAAGGTCAGGTTCAGCTGCAGCAGTCTGACGCTGAG
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Sequence
AR012824
g3971142
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Whitlow,M., Filpula,D. and Shorr,R.
Antigen-binding fusion proteins
Patent: US 5763733-A 7 09-JUN-1998;
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1. .803
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73.9%;
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Best Local S
Matches 499
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TITLE
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                                                                                                                                                            TCTGCAGTCTATTACTGTGCAAG
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                                          TGCTCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGA 237
                                                                                    GCCAGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCC
                                                                                                                   TATCACCTGCAGTGCCAGCTCAAGTATAAGTTCCAATTACTTGCATTGGTATCAGCAGAA 125
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            GCCAGGATTCTCCCCTAAACTCTTGATTTATAGGACATCCAATCTGGCTTCTGGTGTCCC
MASAHIRO
PC C12N
PC C12R
CC Stra
CC topo
CC hypo
CC anti
FH Key
FH Sour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 735)
Ekida,T., Yasukawa,K., Imanaka,T. and Takagi,M.
PRODUCTION OF SINGLE-STRAND FV ANTIBODY
Patent: JP 1997220092-A 1 26-AUG-1997;
TOSOH CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                SO Se de So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP 1997220092-A/1. unidentified.
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DNA encoding a single
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                       165
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JP 1997220092-A/1
26-AUC-1997
15-FEB-1996 JP 1996027622
EKIDA TEIJI, YASUKAWA KIYOSHI, IMANAKA TADAYUKI,
                                                                                                                                                                                                                                                                                                                                                                    topology: Linear;
hypothetical: No;
anti-sense: No;
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                                                                                                                                                                                                                                                                                                                                                                                                      strandedness: Double;
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Location/Qualifiers
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/db_xref="taxon:32644"
192 c 197 g 18
                                                                                                                                                                                                                 44.48;
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Pred. No. 6.5e-87;
1; Mismatches 208;
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Best Local Similarity
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Search completed: May 13, 1999, 09:54:13
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## ALIGNMENTS

DEFINITION vs14f01.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1138201 5' similar to gb: K67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.

AA691311

REYWORDS EST.

SOURCE ORGANISM musculus
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 396)
AUTHORS Geisells. Kucaba T., Lacy, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Title Journal Material, Muse EST Project Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project Washu-HHMI Mouse EST Project Washu-HHMI Mouse EST Project Washington University School of MedicineP

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RESULT
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AA592800
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 344)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N.
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morr Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Mc
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This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                        Mus musculus
                                                                                                                                                        g2406463
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                                                                                                                          house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained from 8 week old mouse. Colon was harvested 72 hours aftuirradiation with 1400 Gys. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
107 c 91 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="1138201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   φ
                 Bowles,M., Dietrich,N., Dubuque,T.,
Le,M., Martin,J., Morris,M.,
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   Underwood, K., Moore, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
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UIN

AI180569 310 bp mRNA
EST UB-UCI-1770
UC70f09.rl Soares mouse mammary gland NbMMG Mus musculus cDNA clone
1431017 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION
(HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene

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FEATURES
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hes 226;
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                                                                                                                       CCACTTATTACTGCCAGCAGTGGAGTCGTA 281
                                                                            GCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGCTGAAGATGCTG
                                                                                                                                                                                     GCAGTGCCAGTTCTACTGTAAGTTACATGCAATGGTAACAGCAGAAGTCAGGTACCTCCC
                                                                                                                                                                                                                  GCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCTCCC 131
CCACTTATTACTGCCAGCATTGGAGTAGTA 344
                                                            GCAGTAGCTCTGGGACCTCCTACTCTCTCACAATCAGCAGAATTGAGGCTGAACATGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theising, B., Wylie, T., Waterston, R.
The WashU-HHMI Mouse E
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       T3/]; double-stranded cDNA was ligated to Eco RI
adaptors [AATTCGGATCCTTG], digested with Not I and clo
into the Not I and Eco RI sites of the modified pT7T3
vector. Library constructed by Bob Barstead."
/db_xref="taxon:10090"
/clone="1050980"
/clone="1050980"
/dev_stage="B weeks"
/dev_stage="B weeks"
/lab_host="DH10B"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                            26.7%;
83.7%;
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                                                                                                                                                                                                                                                                                                                            Score 190.4; DB 22; Pred. No. 1.1e-49;
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                                                                                                                                                                                                                                                                                                                                              Length 344;
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Best Local
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                                                                                                                                                                            448
                                                                                                                                                                                                                                388 TGAGGTGGTGAAGCCTGGAGGTTCAATGAAGAGTATCCTGCAAGACTTCTGGTTACTCATT 447
                                  568
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   205
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                                                                                          ACTTATTAATCCTTACAATGGTGATACTAACTACAACCAGAAGTTCAAGGGCAAGGCCAC 567
                                                                                                                                                                                                            TAAGCTTGTGAAGCCTGG-GGTTCAGTGAAGCTGTCCTGCAAGGCTTCTGGCTACACCTT 84
                  ATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATGGAGCTCCTCAGTCTGACATCTGA 627
                                                                                                                                                                         CACTGGCCACCACCATGAACTGGGTGAAGCAGGCCATGGAAAGAACCTTGAGTGGATTGG 507
                                                                                                                                        CACCAGCTACTGGATGCAGTGGGTAAAAACAGAGGCCTGGACAGGGCATTGAGTGGATCGG 144
AGAGATTGATCCTTCTGATAGCTATACTAACTACAATCAAAAGTTCAAGGGCAAGGCAGC
                                                                                                                                                                                                                                                                                   217;
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AI180569
g3731207
EST.
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Waterston,R.

The WashU-HHMI Mouse EST Project
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of MedicineP
4444 Forest park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
/tissue_type="mammary g
/dev_stage="4 weeks"
/lab_host="DH10B"
a 77 c 85 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="1431017"
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/strain="C57BL/6J"
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Sciurognathi; Muridae; Murinae;
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79.88;
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                                                                                                                                                                                                                                                                                 Score 173.6; DB 3
Pred. No. 2.1e-44;
D; Mismatches 54
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365 GTGCAGCTGCAGGAGTCAGGACCTGAG-GTGGTGAAGCCTGGAGGTTCAATGAAGATATC 423

Matches

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REFERENCE
AUTHORS
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JOURNAL
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                   Local Similarity
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOUSE);,
AI007196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI007196 294 bp mRNA EST 12-JUN-1998 ua73g04.rl Soares 2NbMT Mus musculus cDNA clone 1363158 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 294)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Seq primer: -28m13 rev2 ET from Amersh
High quality sequence stop: 1.
Location/Qualifiers
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
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The WashU-HHMI Mouse
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Fax: 314 286 1810
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                                                                                                                                                                                                       /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
a 68 c 77 g
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                        /sex-"male"
                                                                                                                                                                                          /clone_lib="Soares 2NbMT"
                   22.8%;
76.7%;
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Score 162.4; DB Pred. No. 7e-41; O; Mismatches
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RESULT 5
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435 GTGCAGCTGGTGCAGTCTGGGGGCTGAGGTGAAGAAGCCTGGGGGCCTCAGTGAAGGTCTCC 376
                     365 GTGCAGCTGCAGGAGTCAGGACCTGAGGTGAAGCCTGGAGGTTCAATGAAGATATCC 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown library type
Insert Length: 608 Std Erro
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI201426 461 bp mRNA EST 30-OCT-1998 qs73c06.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943722 3' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); contains Alu repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 461)
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                        93
                                                                          Conservative
                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
/db_xref="taxon:9606"
/clone="TMAGE:1943722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robert_Strausberg@nih.gov
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                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH10B"
132 c 106 g
                                                                                                                                                                                                                                              /sex-"male"
                                                                                                                                                                                                                                                                'clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 461
                                                                                            22.8%;
72.4%;
                                                                Score 162; DB
Pred. No. 1.1e-
0; Mismatches
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No. 1.1e-40;
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EST.
                                                                                                                                                                                                                                                         Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 284. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA569186 387 bp mRNA EST 09-SEP-1997 nm30d10.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061683 similar to gb:L02325 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: David B. Krizman, Ph.I cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 387)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
AA569186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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                   89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert_Strausberg@nih.gov
                                                                                                                                                      /note-"Vector: pamp10; mRNA made from liposarcoma, of made by oligo-dT priming. Non- directionally cloned Size-selected on agarose gel, average insert size (Reference: Krizman et al. (1996) Cancer Research
                                               /clone="IMAGE:1061683"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
                                                                                                                                       56:5380-5383.
                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                       /db_xref="taxon:9606"
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Query Match
Best Local Similarity
Matches 200; Conser

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Score 146; DB 22; Pred. No. 1.1e-35; 0; Mismatches 90

Length 387;

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EST.
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                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov)
MGI:632678
                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.w
This clone is available
                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 345)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Marra, M., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse
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                                                                                                                                                                                                                                                                                                      primer: -28m13 rev2 ET from
h quality sequence stop: 140
                                                                                                                                                                                                                                                                                                                                                                                                 mouseest@watson.wustl.edu
                                                                                                         T 3']; double-stranded count was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead." /db_xref="faxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                          royalty-free through LLNL; contact the image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCACCTGCAAGCCAGTCAGAATGTGGGTACTAATGTAGCCTGGTATCAAGAGAAACCAG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA710970 431 bp mRNA EST 24-DEC-1997 vt93h09:rl Soares mouse mammary gland NDMMG Mus musculus cDNA clone 1178753 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:X70423 M.musculus mRNA for monoclonal antibody heavy chain gamma (MOUSE);, mRNA sequence.
                                                                                                                                                  Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Ix Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                         Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Euther: Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 431)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubl Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free
IMAGE Consortium (info@image.llnl.go
                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                               Waterston, R.
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                                  primer: -28m13 rev2 ET from Amersham
h quality sequence stop: 198.
                                                                                                                                                                                                                                                                                                         WashU-HHMI Mouse
              quality sequence stop:
Location/Qualifiers
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/dev_stage="8 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                          g609691
EST.
                                                                                                                                                                                                                                       EST 06-SEP-199: EST100653 Homo sapiens cDNA 5' end similar to immunoglobulin light chain, V region (GB:L01279) (HT:3043).
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Godayne,J.D., White,O., Sutton,G., Bladke,J.A., Brandon,R.C., Chiu,M.-W., Fine,L.D., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
                                                                                                     Deuterostomia; Chordata; Vertebrata; Gnathostomata; Os
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
                                                                                                                                                                        Homo sapiens
                                                                                                                                                     Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                        human primer=M13 Reverse library=Human Pancreas
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/strain="C57BL/6J"
/note="Organ: mammary gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="1178753"
/clone_lib="Soares mouse mammary
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                                                                                                                                                                                                                                                                                       TGAAGATGCTGCCACTTATTACTGCCAGCAGTG-GAGTCGTAGCCCACCCACCGTTCGGAG 299
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                                                             (HUMAN);,
AA291381
g1939359
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                                                                                                        AA291381 379 bp mRNA EST 08-AUG-1997 zt44902.rl Soares ovary tumor NDHOT Homo sapiens cDNA clone 725234 5' similar to gb:w18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20
Tel: 301869905
Fax: 3018699423
                                             EST
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For clone availability, addi
information related to this
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65.7%;
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Pred. No. 4.7e-27;
1; Mismatches 107;
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                                                                                            273
                                                                                                                                                                                                      543 ACCAGAAGTTCAAGGGCCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACA
                                                                                                                                                                  213 CAGGGAGTTTTCAGGACAGAGTCAGCTTGACCACTGACACATCCACGAATACAGCCTACA
                                                                                                                                                                                                                                                                              363 GTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTCAATGAAGATAT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                          TGGAGCTGAGGAACCTGAGATCTGACGACACACGCCATATATTACTGTGCGAG
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1576 Std Error: 0.00
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Fax: 314 286 1810
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Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
/tissue_type="ovarian tumor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares ovary tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="725234"
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                                                                         118 GCCAGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCC 177
178 TGCTCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCACAGTCAGCAGAGTGGA 237
                                            62 ACCAGGTAAAGCCCCTAAACTCCTGATCTATGNTACATCCACTTTGCAAAGTGGGGTCCC
                                                                                                                                                                                     61 CACAATGACTTGCAGGGCCACCCCAAG---TGTAAGTTACATGCACTGGTATCAGCAGAA 117
                                                                                                                                                                                                                                                              Local
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                                                                                                                                         CACCATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCAGCTATTTACATTGGTATCAGCACAA 61
                                                                                                                                                                                                                                      182;
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AA318377
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The Institute for Genomic
9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser.C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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Eukaryotae; ı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kerlavage, AR
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                            note="Organ: spleen; Vector: pBluescript
ECORI; Site_2: Xho!"
/db_xref="ATCC (inbost):119058"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Spleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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Pred. No. 2.
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kerlavage, AR
Bioinformatics
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                      note="Organ: testis; Vector: pBluescript SK-;
ECORI; Site_2: XhOI"
/db_xref="ATCC (inhost):191658"
/db_xref="taxon:9606"
                                                                                          /sex="male"
                                                                                                                 /clone_lib-"Testis
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g3172923
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
Primates; Catarrhini; Hominidae; Homo

1 (bases 1 to 336)
                                                                                            CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Insert Length: 801 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                                             Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
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Pred. No. 1.:
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/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and

/note="Organ:

/organism="Homo sapiens"

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BASE COUNT
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                                                                                       Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAATTGACCAGCCTGATATTTGAGGACACGCCCATATATTATTGTGCGAG
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EST51505
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g1997722
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                     Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams,M.D.,
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Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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/clone="IMAGE:1602480"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kerlavage, A.R., Fleischmann, R.D.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 CTCCAGGGGAGAAGGTACACAATGACTTGCAGGGCCACCCCAAGTGT-----AAGTTAC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGCACTGGTATCAGCAGAAGCCAGGATCCTCCCCCCAAACCTTGGATTTATACCCACATCC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                              GACTCACCTAGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAATAAAAGGTTCTACCTCTG 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACT 218
                                                                                                                                                                                                                                              AA423447 398 bp mRNA EST 16-OCT-1997 ve80a03.rl Soares mouse mammary gland NDMMG Mus musculus cDNA 832492 5' similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN); gb:M35669 Mouse Ig aberrantly rearranged Kappa-chain mRNA V-J2-C-region, (MOUSE);, mRNA sequence. AA423447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For clone availability, additional sequence and ex information related to this EST, please check the Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockvill
                              Eukaryotae: Metazoa; Chordata; Vertebrata; Mammalia; Euther: Rodentia; Sciurognath; Muridae; Murinae; Mus.

1 (bases 1 to 398)

1 (bases 1 to 398)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubugeis,J., Kucaba,T., Lacy,M., Le,M., Martin,J., Moorris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                              g2102360
                                                                                                                                                                      Mus musculus
                                                                                                                                                                                      house mouse.
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WashU-HHMI Mouse EST Project
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/note="organ: gall bladder; Vector:
Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):147008"
/db_xref="taxon:9506"
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/sex="female"
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Pred. No. 1.4e-24;
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he TIGR Human Gene
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                                                                                                                                                                                                                             229 CAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTCGTAGCCCCACC 288
                                                                                                                                                                                                                                                                    245 CGGGGTCCCTGCCAGGTTTAGTGGCAGTGGGTCTGGGACAGACTTCAGCCTCAACATCCA 304
                                                                                                                                                                                                                                                                                            169 TGGAGTCCCTGCTCGCTTCAGTGGGGGGTGGGGTGTGGGACCTCTTACTCTCTCACAGTCAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                      125 CATCTCCTGCAGAGCCAGCGAAAGTGTTGATAATTCTGGCATTAGTTTTATGAACTGGTT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 AATGACTTGCAGGCCACCCCAAGTGTA-------AGTTACATGCACTGGTA 108
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                                                                                                     GACGTTCGGTGGAGGCACCAAGTTGGAAATCAAA 398
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Seq primer: -28ml3 rev2 ET from Amersham.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex-"male"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH108"
/ab_host="DH108"
/ab_host="DH108"
/ab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 3']; double-stranded CDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="832492"
/clone_11b="Soares mouse mammary gland NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
                   1999, 09:40:43
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Title: Perfect score:

US-08-704-178-1 712

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Scoring table:

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Database

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Score

Match

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T65006 Q55180 T17728 T91615 T91615 Q73678 Q73678 Q85181 T65007 Q81076 Q81076 Q81076

T36463

Q20381 Q66840 Q43292 V63691 T35691 T86646 Q51541 T13740 T36464 V63616 V63616 V63617

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422 356.4 348.4 3348.4 339.6 30.6 30.6 319.3 319.8 317.8 317.8 316.6 316.6 316.6 311.2 313.3 313.2 313.3 313.2 313.3

Q43287 T91614 Q51538 T13737 T36461 Q05713 Q05713 Q05713 Q51539 T13738 T36462 Q05714 Q51540 T13739

Q41069 Q12405 T29058 Q43291 T29059

Monoclonal anti-id Anti-idiotype anti

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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Single chain bindi
TRY104b single cha
18-2-3-TRY202'. S
Coding sequence of
Single chain bindi
18-2-3/TRY202' sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding an a Coding sequence of Single chain bindi TRY59 single chain TRY59. Single poly
                                                                                                                                    Nematode salivary
Mus musculus antib
Coding sequence of
Single chain bindi
18-2-3/TRY59 singl
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PLAP CC49/212 SCA
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OVB3 light and hea
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C The present cDNA sequence codes for a claimed single-chain antibody e23

C designated e23(FY), which binds to erib-2. Monoclonal antibody e23

C was generated by immunising mice with N/erbb-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbb-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbb-2 gpl85 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours. Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Sim
Matches 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5587458-A.
24-DEC-1996.
07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
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Single-chain anti-erbB2 antibody e23(Fv) cDNA.
Single-chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ARON-) ARONEX PHARM INC.
Bird RE, Kasprzyk PG, King
WPI; 97-064831/06.
P-PSDB; WI5185.
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                                  241
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282.2
AGGATCCTCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGC
                                                                                                                                                                                                                                                                                                                                             CACAATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGACCTGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTA
                                                                                                                  TCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCTCACAGTCAGCAGAGTGGAGGC
                                                                                                                                                                                                                                                                                                             CACAATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCC
                                                                                                                                                                                                AGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGTCCCTGC
                                                                                      TCGCTTCAGTGGCGGTGGGTCTGGGACCTCTTACTCTCACAGTCAGCAGAGTGGAGGC
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Pred. No. 4.7e-177;
0; Mismatches 0;
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Best Loc
Matches
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06-JAN-1994.
21-OCT-1992;
30-JUN-1992;
                                                                                         Example; Fig 7; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies no The source of human erbB-2 protein for the prodn. of antibodies no 23 and 21 (055180/R45442; 055181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. I animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;
                                                                                                                                                                                         21-OCT-1992; U08545.
30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY INC.
Kasprzyk PG, King CR;
WPI; 94-025878/03.
P-PSDB; R45442.
Treatment of malignancies over-expressing ERB-[2 - using at Treatment of malignancies which recognise different epitopes o
                                                                                                                                                                                     gp185
                                                                                                                                                                                                                                                                                                                                    Sequence enco
                                                                                                                                                                                                                                                                                                                                                       Q55180 standard;
Q55180;
21-JUL-1994 (fi
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                                                                                                                                                                                                                                                                                                                            monoclonal antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 171
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                             SS.
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                                                    . 68
                                           Pred. No. 3.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      cancer
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cancer therapy; preve
                                            ; DB 1;
3e-176;
es 2;
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WO9607321-A1.
14 MAR-1996.
23-AUG-1995; U10740.
06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
(UABR-) UAB RES FOUND.
CUTIEL DT, Deshane J;
WPI; 96-171307/17.
WPI; 96-171307/17.
P-PSDB; R94020.
                                                                                                                                                                               T17728;
21-MAY-1996 (first e
Anti-erb82 scFv cDNA,
Oncoprotein; erb82; (
intracellular antiboo
Inhibition of proliferation or survival of, esp. malignant erbB2, cells - by introducing nucleic acid mol. encoding antibody homology which is expressed and binds, pref. erbB2, protein intracellularly claim 42; Page 29-30; 48pp; English.

A nucleic acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a signal peptide chain Fv fragment (R94020) that binds a human erbB2 oncoprotein. The anti-erbB2 sFv portion is obtained by PCR using e23scFv
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Matches
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T91615;
22-DEC-1997 (first e
cDNA encoding an anti
Single chain Fv; scFv,
anti-gp130 antibody; i
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibor homologue within e.g. an epithelial carcinoma cell. Intracellular expression of the homologue inhibits surface expression of erbB2 are thereby inhibits cell proliferation and cell survival and decreases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumorigenicity.
Sequence 711
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al Similarity 99.3%;
707; Conservative
                                              (first entry)
                  g an anti-gpl30 antibody
  Fv; scFv; antibody; E. o
ntibody; inclusion body;
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Claim 4; Page 6-7; 9pp; Japanese.

Claim 4; Page 6-7; 9pp; Japanese.

Claim 5; Page 6-7; 9pp; Japanese.

Claim 6; Page 6-7; Page 1: Tollowed single chain Fv (scFv)

Cantibodies which are produced in E. coli. The scFv's are derived

Crom an anti-T3 antibody or an anti-oppia and are produced

Crom an anti-T3 antibody or an anti-oppia and are produced

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15-FEB-1996; 027622.
15-FEB-1996; JP-027622.
(TOYJ) TOSOH CORP.
WPI; 97-474306/44.
P-PSDB; W25784.
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80.2%;
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Best Local Similarity
Matches 574; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunosuppressant polypeptide - has ability to block interleukin-2 response Claim 17; Page 29; 37pp; English.

MAD capable of binding to the gamma chain of the IL-2 recept thus of blocking the IL-2 response, is produced by mouse byt line Gp-2 (FERM BP-4641). DNA encoding the variable region this MAD was expressed in E. coli, yielding Fv(GP-2) with immumosuppressive activity.

Sequence 732 BP; 180 A; 204 C; 182 G; 166 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AJIN ) AJINOMOTO Hamura J, Kanayam Takeshita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1994.
21-APR-1994; 106257.
21-APR-1993; JP-094491.
07-MAR-1994; JP-036065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAb; monoclonal antibody; hybridoma; interleukin-2;
Fv; antibody variable region; GP-2; Fv(GP-2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 94-325948/41.
P-PSDB; R60780.
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               AATGAAGATATCCTGCAAGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGT
                                                               TGAAGGTAAAGGTGTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTGAAGCCTGGAGGTTC
                                                                                                                                                              GAAGCCAGGATCCTCCCCAAACTCTGGATTATAGCACATCCAACCTGGCTTCTGGAGT
                                                                                                                                                                                                                                                                         GAAGCCAGGATCCTCCCCCAAACCTTGGATTTATACCACATCCAACCTKGCTTCTGGAGT
   AGTGAAGCTGTCCTGCAAGGCTTCTGGCTACACATTCACCAGCTACTGGATGCACTGGGT
                                                   CAAAAGCACGCAGGTCAAACTCGAGGAGTCTGGATCTGAGCTGGAGGCCTGGAGCTTC
                                                                                                 CGGTGCTGGGACCAAGCTGGAGCTCAAAGTCGACAAATCCTCAGGATCTGGCTCCGAATC
                                                                                                                                                 GGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCATCGTTCCCCGCTCACGTT
                                                                                                                                                                                                                                                                                                 CACCATGACCTGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTACCAGCA
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78.6%;
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Pred. No. 1.
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L.5e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 732;
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oy mouse hybridoma
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Best Local S
Matches 511
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Q55181;
21-JUL-1994
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06-JAN-1994.
21-OCT-1992; 1
30-JUN-1992; 1
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Example; Fig 8; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies not and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
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Treatment of ma
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WPI; 94-025878/03.
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(MOLE-) MOLECULAR ONCOLOGY
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AGTGGCGGTGGGGTCTGGGACCTCTTACTCTCACAGTCAGCAGAGTGGAGGCTGAAGAT
                                             ACTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCC
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11; Conservative
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antibodies w
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oding the single chain anti-erbB2 antibody, Ab
anti-erbB1 antibody; cancer therapy; preventic
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lich recognise different
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Pred. No. 2.3e-103;
1; Mismatches 131;
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PT Single chain antibodies specific for erbB-2 protein, gpl85 - with PT labels or cytotoxin, useful for detection and treatment of tumour PT cells expressing this protein
PS Example 9; Columns 27-30; 28pp; English.

CC The present cDNA sequence codes for a claimed single-chain antibody e21

CC designated e21(FV), which binds to erbB-2. Monoclonal antibody e21

CC was generated by immunising mice with N/erbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 coding for the heavy- and light- chain variable regions were then complified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro cliswhich overexpress the erbB-2 gpl85

CC marker, e.g. breast, ovarian and non-small cell lung carcinomas, cand, when coupled to a cytotoxic agent, to treat such tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1997 (first entry)
Single-chain anti-erbB2 antibody e21(Fv) cDNA.
Single chain antibody; variable region; light chain; heavy
breast cancer; ovarian cancer; non-small cell lung carcinom
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bird RE, Kasprzyk PG, WPI; 97-064831/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1991; 772270.
07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T65007 standard;
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T binding domains for separate targets joined by helical peptide,
T useful e.g. for diagnosis and treatment
S Example 1; Fig 11; 50pp; English.
C The VL and VH sequences of the anti-CD3 hybridoma G19-4 were
amplified by PCR methods. A gene fusion was constructed from the
C two amplified domains and a (G1y4Ser)3 linker. The amino
C terminus of the VL-VH fusion cassette was fused at the Sall site to
C the L6 light chain variable region leader peptide and the
C carboxy-terminus was fused directly to the hinge region of the PC
C domain at the Bcl1 site and/or to a short "helical" peptide linker
C to construct the bispecific CD3-L6FvIg antibody derivative. The
C the helical liker fort included in frame to the opposite end of
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31-JAN-1994, 300692.
31-JAN-1994, 300692.
01-FEB-1993, US-013420.
13-SEP-1993, US-121054.
13-SEP-1993, US-121054.
(BRIM ) BRISTOL-MYERS SQUIBB Comparing the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_rna
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WPI; 94-250885/31.
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                                                                                                                                                                                                                                                                                                                                                                                                       ----GTGCAGCTGCAGGAGTCAGGACCTGAGGTGGTG----
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223 C; 228 G;
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                                                                                       Complete the containing a target binding molety capable of binding to a complex receptor (SECR), and a nucleic acid binding to a complex receptor (SECR), and a nucleic acid binding molety. This can be used in a method for delivering an oligonucleotide to a commandian cell. The method comprises conjugating the target binding to a complete to a nucleic acid binding molety to form a carrier and coupling the carrier to an expression vector encoding one or more gene products to form a pharmaceutical composition. A mammalian cell having on its conditions allowing binding to the receptor resulting in delivery of the pharmaceutical composition to the interior of the cell. The composition and method are used for the introduction of exogenous genetic material into target host cells expressing SECR on their surface. The nucleic acid may encode a functional wild-type or mutant gene or may be an antisense comprosed to a cell surface via the SECR binding molety. The nucleic acid can be compacted at high concentrations with the carrier molecule at a critical salt concentration. The such complexes comprose only of more expression.
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Query Match
Best Local S
Matches 514
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11-DEC-1997; U09858.
03-JUN-1997; U09858.
03-JUN-1996; US-656906.
(UYCA-) UNIV CASE WESTERN RESERVE.
Davis PB, Ferkol TW, Ziady A;
WPI; 98-041783/04.
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Key
CDS
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Fusion protein; SC single chain Fv/protamine fusion protein; SECR;
exogenous gene; serpin enzyme complex receptor; gene therapy; target;
binding molety; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Delivering compacted exogenous nucleic acid to cells - by the serpin enzyme complex receptor, used in gene therapy Example 9; Pages 120-121; 188pp; English.

This DNA encodes an anti-human SC single chain Fy/protamine
                                                                              Sequence
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Score 350.4; Pred. No. 2.5e
0; Mismatches
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                            EP-621338-A.
26-0CT-1994; 106257.
21-APR-1994; 106257.
21-APR-1994; JP-034491.
07-MAR-1994; JP-036065.
(AJIN ) AJINOMOTO KK.
Hamura J, Kanayama Y, N
Takeshita T;
WPI; 94-325948/41.
                                                                                                                                    Q73679 standard; DNA; 729 BP.
Q73679;
Q9-MAY-1995 (first entry)
FV(GP-4) immunosuppressive.
MAD; monoclonal antibody; hybridoma;
FV; antibody variable region; GP-4; F
                      P-PSDB; R60781.
                                                                                                                            immunosuppressive;
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Immunosuppressant polypeptide
interleukin-2 response
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Best Local :
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041069 standard; DNA; 848 BF
041069;
25-AUG-1993 (first entry)
26-10 sFv coding sequence.
Heavy; light; variable; VH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 29; 37pp; English.

MAb capable of binding to the gamma chain of the IL-2 receptor, and thus of blocking the IL-2 response, is produced by mouse hybridoma line GP-4 (FERM BP-4640). DNA encoding the variable region of this MAb was expressed in E. coli, yielding Fv(GP-4) with immumosuppressive activity.

Sequence 729 BP; 199 A; 169 C; 182 G; 179 T;
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                                                                                                                                                      CGTCTC
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71.5%;
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Pred. No.
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No. 8e-84;
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antidigitoxin; monoclonal;

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This sequence encodes a single chain Fv molecule which contains the heavy and light variable portions (VH and VL) of antidigitoxin monoclonal antibody (MAD) 26-10, a signal sequence and a linker monoclonal antibody (MAD) 26-10, a signal sequence and a linker between the two variable regions. This sequence was used in the construction of an expression-secretion system for the production of biologically active Fv fragments. The system also contains a DNA sequence encoding the T7 promoter. The secretion expression vector was produced by polymerase chain reaction (see also Q41070-81). Fv fragments comprising only the VH or VL regions, and single chain concluses may be used to specifically bind one or more of the same antigens as the full length antibody from which they are derived. Sequence 848 BP; 209 A; 216 C; 219 G; 204 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 459
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Key
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Anthony JG, Ng SC,
WPI; 93-152491/18.
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expression-secretion system; T7 promoter; signal peptide; molecule
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18-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                       TCCAACCTKGCTTCTGGAGTCCCTGCTTCAGTGGCGGTGGGTCTGGGACCTCTTAC
                               AGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAATAAAAGGTTCTACCTCT
                                                                                                                                                                                                                                               eal Similarity
459; Conser
TTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATT
                                                                                                      GGTTCTGGTAAATCTTCTGAAGGTAAA-----
                                                                                                                                                                           ACACATGTTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGGTGGTTCT
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nilarity 72.9%;
Conservative
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US-777709.
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81. .419
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"26-10 VH
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Pred. No. 2.4e
0; Mismatches
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                                                                                             Query Match
Best Local Sin
Matches 479;
                                                                                                                                                                                                                                                                                                                                          US7463111-A.
28-MAY-1991.
11-JAN-1990;
11-JAN-1990;
                                                                                                                                                     Disclosure; Fig 3; 26pp; English.

The sequence is an Ndel-Hindlil fragment encoding the L and H chains of murine MAD OVB3, joined together via a linker. The sequence is present in clone povB3158-1 in which the 3' end is linked to the 5' end of the coding sequence for PB40, a a Pseudomonas exotoxin lacking domain I. The protein expressed by the clone can be used to kill specific target cells.

Sequence 738 BP; 181 A; 193 C; 192 G; 172 T;
                                                                                                                                                                                                                                                     Rapid cloning of antibody genes as single chain immuno-toxins by fusing genes with DNA encoding cytotoxic molecules, to kill target cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q12405;
16-SEP-1991
                                                                                                                                                                                                                                                                                           WPI; 91-200877/27.
P-PSDB; R12798.
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Synthetic.
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Immunoglobulin; immunotoxin;
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CACCATGACCTGCAGTGCCATCTCAACTGTAAGTTACATGCACTGGTACCAGCAGAAGTC
           CACAATGACTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAGAGCC
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                                               ATGGAAAATGTGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGT
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                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                            0; 133066.
0; US-463111.
T INST OF HEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exotoxin;
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          /label linker
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7. .327
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/label-
                                                                                                                                                                                                                                                                                                                                                                                        /label- heavy chain
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                                                                                                                                                                                                                                                                                                                              HEALTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; variable region; PE40;
                                                                                             Score 320.6; DB 1;
Pred. No. 1.9e-76;
1; Mismatches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       818
                                                                                              Indels
                                                                                                                     Length
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                                                                                             Gaps
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Filputa D. D. P. PSDB; R97380.

P-PSDB; R97380.

New antigen binding proteins contg. immunoeffector or cytolytic peptide - attached to variable regions of antibody light or heavy chain, useful in diagnosis and in destroying cancer cells Example 1; Fig 4A-B; 72pp; English.

A novel DNA construct (T29058) codes for a single-chain antigen-binding fusion protein (R97380) comprising the light chain variable region (VL) of monoclonal antibody Cd49 linked to the CC49 VH region via a spacer peptide (R97379). With a C-terminal
                                                                                                                                                                                                     WO9611955-A1.
25-APR-1996.
13-OCT-1995; U12840.
13-OCT-1994; US-323445.
(ENZO-) ENZON INC.
Filpula D. Shorr R, Wh
                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                   T29058;
03-OCT-1996 (first entry)
CC49/212 SCA PLAP DNA construct.
Single-chain antigen-binding fus
                                                                                                                                                                                                                                                                                                                                                                                      Single-chain antigen-binding fusion procytostatic; phospholipase A activating therapy; monoclonal antibody; CC49; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T29058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGACCAAGCTGGAGCTCAAAGAGGGTAAATCCTCAGGATCTGGCTCCGAATCCAAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                       1. .789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         797
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                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                         linker-VH-PLAP
                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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in; PLAP;
                                                                                                                                                                                                                                                                                                                                                                                                                        immunoeffector;
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RESULT
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Best Local Similarity 72.0%;
Matches 447; Conservative
                                                                                                                                                                                                                                                                                                        Q43291 stand
Q43291;
27-SEP-1993
                                                                                                                                        Synthetic.
Key
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Sequence 797 BP; 196 A; 203 C; 195 G; 203
                                                                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                           Sequence encoding
                                                                                                                                                                                                                      Antibody; multivalent;
                                                                                                                                                                                               linker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACCATGCAATTCACTGGGTGAAACAGAACCCTGAACAGGCCTGGAATGGATTGGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTTCTGGTAAATCTTCTGAAGGTAAAGGT---GTGCAGCTGCAGGAGTCAGGACCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTCGTAGCCCACCCACGTTCGGAGGGGGGGTCCAAGCTGGAAATAAAAGGTTCTACCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCAACCTKGCTTCTGGAGTCCCTGCTTCAGTGGCGGTGGGTCTGGGACCTCTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAACCTCGGTCACCGTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGCAGACAATCCTCCAGCACTGCCTACGTGCAGCTCAACAGCCTGACATCTGAGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCGCTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGGGACAGATTTC
                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                               ss.
                                                                                                                                                                                                                                                            (first entry)
ding divalent CC49/212 single-chain antigen-binding
                       /*tag=
1. .339
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/product=
                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               DNA; 1460
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CC49
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; Pred. No. 5.2e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             723
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10-JUN-1993.
20-NOV-1992; U09965.
25-NOV-1991; US-796936.
(ENZO-) ENZON INC.
Bird RE, Filpula D, Ha:
Wood JF;
WPFI; 93-19699/24.
                                                                                                                                                                                                                                                                                                                                                                                    antibody.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   New multivalent antigen-binding protein e.g. contgregions - useful in diagnosis, for destroying blood targetting cytotoxic agents or enzymes to tumour ce Example; Fig 16A; 118pp; English.

The number 212 refers to a 14-residue linker. CC49
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                                                                                    GGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTT
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 ACTGCAGACAAATCCTCCAGCACTGCCTACGTGCAGCTCAACAGCCTGACATCTGAGGAT
                                              ATTAATCCTTACAATGGTGATACTAACTACAACCAGAAGTTCAAGGGCAAGGCCACATTT
                                                                         GACCATGCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGGATAT
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1066. .1107
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375. .426
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1108. .1449
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Filpula D, Shorr R,
WPI; 96-221949/22.
P-PSDB; R97381.
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T29059;
03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antigen binding proteins contg. immunoeffector or cytolytic peptide - attached to variable regions of antibody light or heavy chain, useful in diagnosis and in destroying cancer cells Disclosure; Page 39-40; 72pp; English. A novel DNA construct (T29059) codes for a single-chain antigen binding fusion protein (R97381) comprising the light chain variable region (VL) of monoclonal antibody CC49 linked to the CC49 VH region via a spacer peptide (R97379) and with an N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLAP CC49/212 SCA DNA construct.
Single chain antigen-binding tasion protein;
cytostatic; phospholipase A activating prote:
therapy; monoclonal antibody; CC49; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen-binding capability of PLAP. Sequence 803 BP; 198 P
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13-OCT-1995; U12840.
13-OCT-1994; US-323445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phospholipase A activating protein (PLAP) immunoeffector peptide (R97368). It can be used to produce the fusion protein in transformed host cells. The fusion protein combines the tumour artigen-binding capability of CC49 with the immunoeffector functive
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Pred. No. 1.1e-75;
1; Mismatches 143;
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Search completed: May 13, 1999, 09:55:24 Job time: 1182 sec

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ACCESSION 132407
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REFUNCTION 91823198
REYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 720)
AUTHORS King,C.Richter, Rasprzyk,P.G. and Bird,R.E.
TITLE Anti-erbB-2 antibodies, combinations thereof, and therapeutic and diagnostic uses thereof
JOURNAL Patent: US 5587458.
FEATURES SOURCE 1.720
BASE COUNT 184 a 178 c 179 g 179 t
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Query Match

100.0%;

Score 720;

DB 6;

Length 720;

Local Similarity 100.0%; hes 720; Conservative

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Pred. No. 1.: , Mismatches

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                                           Unclassified.

1 (bases 1 to 711)

King,C.R.chter, Kasprzyk,P.G. and Bir
King+C.R.chter, Kosprzyk,P.G. and Bir
Anti-erbB-2 antibodies, combinations
diagnostic uses thereof
Patent: US 5587458-A 1 24-DEC-1996;
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GenBank staff at the National Library of Medicine entry [NCBI gibbsq 108547] from the original journ This sequence comes from Fig. 1.

Location/Qualifiers
                                                        1 (bases 1 to 711)
Batra, J.K., Kasprzyk, P.G., Bird, R.E.,
Recombinant anti-erbB2 immunotoxins co
Proc. Natl. Acad. Sci. U.S.A. 89 (13)
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0; Mismatches 131;
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Kanayama,Y.,

Sugamura

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                                                                          AATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCGGCCTACCTTCAGC 601
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Sequence
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/translation="MDLOLTQSPAILSASPGEKVIMICRATPSVSYMHWYQQKPGSSP/translation="MDLOLTQSPAILSASPGEKVIMICRATPSVSYMHWYQQKPGSSPKPWITTSNLASGVPARFSGGGSGTSYSLTVSRVEADDATYYCQQWSRSPPTEGGS
KLEIKGSTSGSGKSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQS
HGKNLEWIGLINFYNGOTNYNOKFKGRATFTVDKSSSTAYMELLSLTSEDSAVYYCAR
RVIDWYEDVWGAGTTYTYS"
182 c 190 g 164 t
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/gene="anti-erbB2 imr
/note="This sequence
/codon_start=1
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/db_xref="taxon:10095"
1. .711
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/gene="anti-erbB2 imnmunotoxin
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79.6%;
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patent
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Pred. No. 3.4e-123;
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                                                                                TACGATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACACCATCCTCCAGCACAGCC
                                                                                                                                             TATGACCCGAAATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCCGGCC
                                                                                                                                                                                                                                 CTGTCCTGCAAGGCTTCTGGCTACACATTCACCAGCTACTGGATGCACTGGGTGAAGCAG
                                                                                                                                                                                                                                              TTGTCCTGCAAAGCTTCTGACTTCAACATTAAAGACTATTATATCCACTGGGTGAAGCAG
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                                     AGCCGGAACTGGGTCTACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC
                                                            TACTACTATAGTGCTACTATGCTATGTACTACTGGGGTCAAGGAACCTCGGTCACCGTC 711
                                                                                                                                                                                  AGGCATGGACAAGGCCTTGAGTGGATTGGAAATATTTATCCTGGTAGTGGTAGTACTAAC
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557; Conservative
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g1821826
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Interleukin-2 receptor
Patent: US 5582826-A 1 10-DEC-1996;
Location/Qualifiers
1. 732
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Monoclonal antibodies which
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Shimamura, T., Hamuro, J.,
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Pred. No. 9.3e-123;
0; Mismatches 160;
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Patent number JP 1995313188-A/1,
AJINOMOTO CO INC, SUGAMURA KAZUO,
                                                                                                                                                 Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                        Mus
                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding a receptor gamma
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08-OCT-1997
                                                                                              Sequence
                                                                                                                    source
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                                                         Local Similarity
nes 557; Conserv
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SUGAMURA KAZUO, TAKESHITA TOSHIICHI
C12P21/08,61839/395,861839/395,C12N1/21,C12N5/20,
C12N15/13//C12N15/06,
(C12P21/08,C12R1:19),(C12P21/08,C12R1:91),(C12N1/21,C12R1:19);
                           ATGCAGCTGACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCACCATG
                                                                                                                                                                                                                                                          Mus sp. (mouse)
yp 195313188-A/1
05-DEC-1995
21-APR-1994 JP 1994082836
21-APR-1993 JP 93P 94491, 07-MA
SHIMAMURA TOSHIAKI, HAMURO JUNJI,
        ACCTGCAGTGCCAGCTCAAGTGTA-----AGTAACATGCACTGGTATCAGCAGAAGTCA 114
ACCTGCACTGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTACCAGCAGAAGCCA
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hi; Muridae;
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                                                                                                                                                                                                                 Double;
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/cell_type-"hybridoma"
/cell_line-"GP-2"
1. 732
/product="anti-IL-2 rec
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76.7%;
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A rapid method of cloning functional variable-region in Escherichia coli as single-chain immunotoxins
Proc. Natl. Acad. Sci. U.S.A. 87, 1066-1070 (1990)
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E kidda,T., Yasukawa,K., Imanaka,T. and Takagi,M...

FRODUCTION OF SINGLE-STRAND FV ANTIBODY

Patent: JP 1997220092-A 2 26-AUG-1997;

TOSOH CORP

OS None

OC Artificial sequences.

PN JP 1997220092-A/2

PD 26-AUG-1997

PF 15-FEB-1996 JP 1996027622

PI EKIDA TEIJI, YASUKAWA KIYOSHI, IMANAKA TADAYU

MASAHIRO

PC C12N15/09,C12N1/21,C12P21/08,(C12N1/21,C12R1:P);

CC C12N15/09,C12N1/21,C12P21/08,(C12N1/21,C12R1:P);

CC C12R1:19);

CC strandedness: Double;

CC cantisense: No;

FH Key Location/Qualifiers

FH Key Location/Qualifiers

FH Source /organism='Antificial sequence
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/db_xref="taxon:32644"
193 c 190 g 16
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Pred. No. 6.9e-108;
0; Mismatches 187;
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IgG3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-MAY-1997) | Agricultural University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; Metazoa; Chordata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae; N
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748 /note="Heavy chain i
coding sequence"
775 .807
                                                                                                                                                                /note="814..8
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                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                               /translation="MAQVDGDIQMTQSPPSIPYSIGDQASISCRSSQSIVHSKGNTYLEWFLQKPGQSPKLIKGSUSVETSGVPDKFSGSGSGTDFTKISKBAEDLGVYYCFQGSHVPYTFGGGTKLEIKGGGSGGGGSGGGGSGVPQLQESGAELVRSGASVKLSCTASDINGVYTHWKQRPEQGLEWIGWIDPENGGTDYAPKFQGKATMTADTSSNTAYLQLSS
                                                                                                                                   814. .825
/note="KDEL coding
196 c 228 g
                                                                                                                                                                                                                                                                                                                                                                                                     /product="IgG3/kappa antibody"
/db_xref="PID:e1167936"
/db_xref="PID:g2108313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/note="recombinant gene"
/db_xref="taxon:10090"
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Box 8123, Wageningen 6700
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                                                              2 (bases 1 to 822)
Schouten,A., Roosien,J., de Boer,J.M., Wilmink,A., Ross Bosch,D., Stiekema,W.J., Gommers,F.J., Bakker,J. and Sc Improving scFv antibody expression levels in the plant FEBS Lett. 415 (2), 235-241 (1997)
                                                                                                                                                  Direct Submission
Submitted (07-MAY-1997) Dept.
Agricultural University, P.O.
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/organism="Mus musculus"
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Box 8123, Wageningen 6700
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                                                                                                                                         GATGGATTCATCCTGAGAATGGTAATACTGTATATGACCCGAAATTCCAGGGCAAGGCCA 559
                                                                                                                                                                                                      TTAAAGACTATTATATCCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAATGGATTG
                                                                                                                                                                                                                                                    CAGAGCTTGTGAGGTCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGACTTCAACA
                                                                                                                                                                                                                                                                      TTGAGCTTGTCCGAGGAGGGGCCTTAGTCAAGTTGTCCTGCAAAGCTTCTGACTTCAACA
                                                                                                                                                                                                                                                                                                                                     GTAAATCTTCTGAAGGTAAAGG------TGTGCAGCTGCAGCAGTCTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGATCAGCAGCATGGAGGCTGAAGATGCTGCCACTTATTATTGTTATCAGGGGAGTGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGGTTCCTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACC
                                                            GATGGATTGATCCTAAGAATGGTGATACTGATTATGCCCCGAAGTTCCAGGGCAAGGCCA
                                                                                                                                                                                                                                                                                                                 GTTCCGGTGGTGGAGGCTCCGGAGGCGGAGGATCCGAGGTCCAGCTGCAACAGTCTGGGG
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 AGGACACTGCCGTCTATTACTGTAGTGCCTATGGTGACTTCGACGCCTAC
                             AGGACACTGCCGTCTATTACTGCTGCTTCTTATTACTACTATAGTGCTTAC
                                                                                                                                                                                      TTAAAGACTACTATATACACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTG
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436; Conser
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769. 801
/note="c-myc tag coding sequence"
808. 819
/note="KDEL coding sequence"
a 203 c 221 g 184 t
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/translation="MDVMTOTPLSLPVSLGDQASISCRSSQTILHSNGNTYLEWFLQ
/translation="MDVMTOTPLSLPVSLGDQASISCRSSQTILHSNGNTYLEWFLQ
KPGQSPKLLIIKVSNRFSGVPDRFSGSGSGSTDFTLKISRVEAEDLGVYYCFQGSHVPY
TFGGCTKLEIKGSGGGGSGGGGSGGGGSEVQLQQSGAELVRSGASVKLSCTASDFNI
KDYYIHWVKQRPEQGLEWIGWIDPKNGDTDYAPKFQGKATMTADTSSNTAYLQLSSLT
KDYYIHWVKQRPEQGLEWIGWIDPKNGDTDYAPKFQGKATMTADTSSNTAYLQLSSLT
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/note="Linker peptide coding sequence"
394. .741
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742. .756
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/product="IGG1/kappa antibody"
/db_xref="PID:e1167935"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
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Pred. No. 1.5e-90;
0; Mismatches 139;
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Best Local S
Matches 491
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                                                                                                                                                  GAAGATGCTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCG
                                                                                                                                                                                                        CGCTTCAGTGGCAGTGGGTCTGGAAACTCTTACTCTCTCACGATCAGCAGCATGGAGGCT 234
                                                                                                                                                                                                                                              GGATTCTCCCCTAAACTCTTGATTTATAGGACATCCAATCTGGCTTCTGGTGTCCCAACT
                                                                                                                                                                                                                                                                                                               ACCTGCAGTGCCAGCTCAAGTGTAAG-----TAACATGCACTGGTATCAGCAGAAGTCA 114
 TTGTCCTGCAAAGCTTCTGACTTCAACATTAAAGACTATTATATATCCACTGGGTGAAGCAG
                         TCCGAGGTCAAGCTGCAGGAGTCTGGGGGGAGGCTTAGTGAAGCTTGGCGGGTCCCTGAAA
                                                     ---GGTGTGCAGCTGCAGCAGTCTGGGGGTTGAGCTTGTCCGAGGAGGGGGCCTTAGTCAAG 411
                                                                              GGGACAAAGTTGGAAATAAAAGGTTCTACCTCCGGATCTGGTAAATCTTCTGAAGGTAAA
                                                                                                                                    GAAGATGTTGCCACTTACTACTGCCAGCAGGGTAGTAGTATACCGCTCACGTTCGGTGCT
                                                                                                                                                                                        CGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATTGGCACCATGGAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                            491;
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OC JP 11
PD 26-A
PD 26-A
PD EKID
PI EKID
PI EKID
PC C12N
MASAHIRO
MCSC C12N
PC C12R
CC Stra
CC topo
CC antil
FH Key
FH Sour
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Ekida, T., Yasukawa, K., Imanaka, T. and Takagi, M.
PRODUCTION OF SINGLE-STRAND FV ANTIBODY
Patent: JP 1997220092-A 1 26-AUG-1997;
TSOOH CORP
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JP 1997220092-A/1.
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DNA encoding a single chain Fv antibody of anti-T3 antibody
E13598
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Artificial sequences.
JP 1997220092-A/1
26-AUG-1997
15-FEB-1996 JP 1996027622
ELIDA TEIJI, YASUKAWA KIYOSHI, IMANAKA TADAYUKI,
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism='Artificial sequences'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:32644"
192 c 197 g
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Pred. No. 3.6
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es 226;
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Best Local Similarity 69.0
Matches 504; Conservative
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                                                                                       CAGTGGCAGTGGGTCTGGAAACTCTTACTCTCACGATCAGCAGCATGGAGGCTGAAGA
                                                                                                                     GCTCACCCAGTCTCGAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCACCATGACCTG
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                 AAAGTTGGAAATAAAAGGTTC---TACCTCCGGATCTGGTAAATCTTCTGAAGGTAAAGG
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Sequence
I08678
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Ladner, R.C. and Bird, R.E.
SINGLE POLYEEPTIDE CHAIN BINDING MOI
Patent: WO 8801649 A 10 10-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                Unknown
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1. .741
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188 c 192 g
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Pred. No. 1.4e-88;
0; Mismatches 208;
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                                                        CAGTGGCAGTGGGTCTGGAAACTCTTACTCTCACGATCAGCAGCATGGAGGCTGAAGA 239
                                                                                                     CTCCCCCAAACTCTGGGTTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGTCGCTT 179
                                                                                                                                     CAGGGCCAGCTCAAGTGTAAGTTCCAGTTCCAGTTACTGGTTCCAGCAGAAGTCAGGTGC 131
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TGCTGCCACTTATTACTGCCAGCAGTACAGTGGTTACCCACTCACGTTCGGTGCTGGGAC
                                            CAGTGGCAGTGGGGTCTGGGACCTCTTACTCTCACAATCAGCAGTGTGGAGGCTGAAGA
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Ladner,R.C. and Bird,R.E.
SINGLE POLYDEPTIDE CHAIN BINDING MOI
Patent: WO 8801649-A 12 10-MAR-1988
Location/Qualifiers
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                                                                                             AACCTCAGTCACCGTCTCCTAA 753
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              AAATCTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCATCAAGG
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Sequence 3
131036
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Takeshita T.;
Takeshita T.;
"IMMUNOSUPPRESSIVE AGENT";
"IMMUNOSUPPRESSIVE AGENT";
Patent number JP 199531318'
Patent number JP 199531318'
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AJINOMOTO
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Eukaryota; Metazoa; Chordata; Vertebrata;
Sciurognathi; Muridae; Murinae; Mus.
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Mus sp. (mouse)
JP 1995313188-A/2
05-DEC-1995
21-APR-1994 JP 1994082836
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SHIMAMURA TOSHIAKI, HAMURO JUNJI, NAKAZAWA HARUMI,

KANAYAMA YUKA,

SUGAMURA KAZUO, TAKESHITA TOSHIICHI

C12P21/08,AG1K39/395,AG1K39/395,C12N1/21,C12N5/20,

C12N15/13//C12N15/06,

(C12P21/08,C12R1:19),(C12P21/08,C12R1:91),(C12N1/21,C12R1:19);

Key

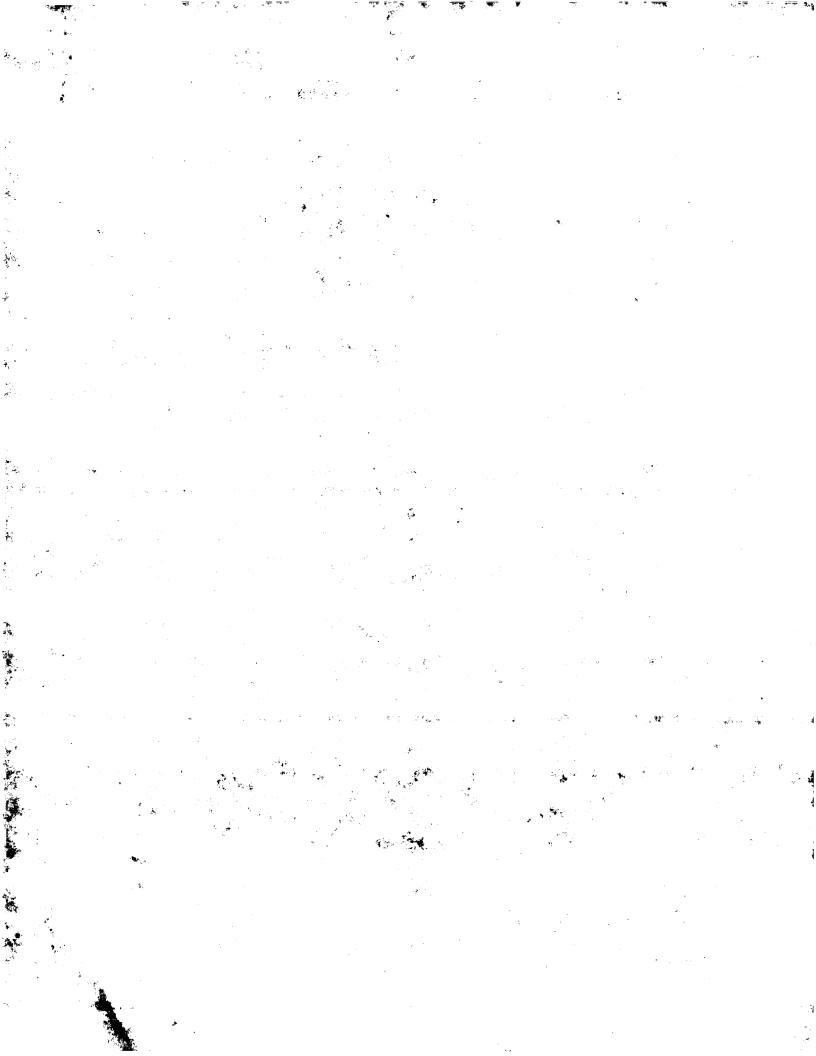
Location/Qualifiers
                                                                     ACCAGAATTTCAAGGACAAGGCCAGCTTGACTGAGATAAGTCCTCCAGCACAGCCTAC
                                                                                                                                CCTGAACAGGGCCTGGAATGGATTGGATGGATTCATCCTGAGAATGGTAATACTGTATAT
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                       ATGGAGCTCCACAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGAGAGAAT
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                                              CTTCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTTCTTATTAC
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/organism="Mus
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/cell_type="hybridoma"
/cell_line="GP-4"
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                              GCAGAAACCAGGACAGTCTCCTGAACTTCTGGTATACTTTGCATCCACTAGGGAATCTGG
                                                         GCAGAAGTCAAGCACCTCCCCCAAACTCTGGGTTTATGACACATCCAAACTGGCTTCTGG 164
                                                                                           CAAGTCCAGTCAGAGTCTTTTAAATAGTAGCAATCAAAAGAACTATTTGGCCTGGTACCA 128
                                                                                                            CAGTGCCAGCTCAAGTGTAAGTAACA------TGCACTGGTATCA 104
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constructed from variable light and heavy chain
monoclonal antibody DA4.4, 3' end of cds.
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Nagle,J.W. and Filpula,D.
Production of engineered
Escherichia coli
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90; Conservative
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/transl_table=1
/transl_table=1
/function="binds human Igm"
/product="fusion protein"
/db_xref="pin:9310740"
/db_xref="pin:9310740"
/translation="bywmyGspssLAMSVGOKVTMSCKSSOSILINSSNOKNYLAWYQO
/translation="bywmyGspssLAMSVGOKVTMSCKSSOSILINSSNOKNYLAWYQO
/translation="bywmyGspsschotholingsvonabDLADYFCQOHYSTPF
TFGSGTKLEIKGSTSGSGKSSGVDTGLQDFGAEFVKPGAPVKLSCKASGYPFTTYW
VNMXCREFRGLEMIGRIDFYDSETLYNOKFKDKATLTVDKSSTAYIQLSSLTSEDS
AVYYCARETYDYPFAYWGQGTLVTVS"
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/db_xref="taxon:29278"
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Pred. No. 3.2e-81;
0; Mismatches 216;
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TGCTTCTTATTACTACTATAGTGCTTACTATGCTATGTACTACTGGGGTCAAGGAACCTC 701
                                                        TAATACTGTATATGACCCGAAATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTC 581
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AA592800 vo25g11.r
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482 yj83c03.r 81192 nd38b11 68604 go47a1C 10970 vt93h09 342 EST77181	AI180569 uc70f09.r AI201426 gc73c06.x AA569186 nm30d10.s AA569186 nm30d10.s AA669186 nm30d10.s AA077111.r AA456778 zw27f11.r AA456778 zw27f11.r AA710291 vt53a04.r AA359311 EST100400 AA300732 EST13047 AA295391 zt44907.s AA351439 ng69c07.s AA357405 EST78511 AI233978 EST23066 R69532 y782d09.r1 AA3767405 EST78511 AI233978 EST23066 R69532 y782d09.r1 AA371347 ve80a03.r AA37147 zest2624.r AA313377 EST20620 AA313378 EST34279 AA335086 EST39457 AA30561 EST14279 AA335086 EST39457 AA30561 EST14181 R67559 y142h11.r1 AA300582 EST13427 AA170256 ms87910.r T29112 EST69384 H0 H62115 yu40h01.r1 T29916 EST99971 H0 AA300891 EST14031 AA300891 EST14031 AA300891 EST14031 AA3100788 EST13548	

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Clone 1138201 5' similar to gb:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.

CCESSION
AA691311
TD
GURCE
CORGANISM
Mus musculus
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

EFERENCE
1 (bases 1 to 396)
AUTHORS
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thetsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
TITLE
JOURNAL
The Washu-HHMI Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP

ALIGNMENTS

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AUTHORS
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AA592800
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                                                                                                                                                                             AA392800 344 bp mRNA EST 17-SEP-1997 vo25gll.rl Barstead mouse irradiated colon MPLRB7 Mus musculus clone 1050980 5' similar to gb:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 344)
Marfa, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morr Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Mc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@image.linl.gov) for fv
                                                                                                            Mus musculus
                                                                                                                             house mouse
                                                                                                                                                                g2406463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adaptors [AATTCGCATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

(db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="1138201"
/clone=lib="Barstead mouse
/dev_stage="8 weeks"
/lab_host="DH10B"
107 c 91 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtai
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   , Martin,J., Morris,M.,
Underwood,K., Moore,B.
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                                   Dietrich, N.,
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DEFINITION

AI180569 310 bp mRNA DEST 08-OCT-1998 uc70f09.r1 Soares mouse mammary gland NbMG Mus musculus cDNA clone 1431017 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene

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                                                                                            GCAGTAGCTCTGGGACCTCCTCTCTCACAATCAGCAGAATTGAGGCTGAACATGCTG
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                                       CCACTTATTACTGCCAGCATTGGAGTAG
                                                               CCACTTATTATTGTTATCAGGGGAGTGG 272
                                                                                                                    GCAGTGGGTCTGGAAACTCTTACTCTCTCACGATCAGCAGCATGGAGGCTGAAGATGCTG 244
                                                                                                                                               CCAAAACATGGATTTATGATACATCTAAACTGGCTTCTGGAATCCCTGCTCGCTTCAGTG
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:582556
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/strain="FVB/N"
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D; Mismatches 41
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                                  CCGAAATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCGGCCTACCTT 597
                                                                                            GAACAGGGCCTGGAATGGATTGGATGGATTCATCCTGAGAATGGTAATACTGTATATGAC
                                                                                                                                              TGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGTAAAACAGAGGCCT
                                                                                                                                                                     TGCAAAGCTTCTGACTTCAACATTAAAGACTATTATATCCACTGGGTGAAGCAGAGGCCT 477
                                                                                                                                                                                                                                                          GTGCAGCTGCAGCAGTCTGGGGGTTGAGCTTGTCCGAGGAGGGGCCCTTAGTCAAGTTGTCC 417
 CAMAAGTTCAAGGGCAAGGCAGCATTGACTGTAGACACATCCTCCAGCACAGCCTACATG
                                                                     Mus musculus

Eukaryota, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 310)

1 (bases 1, to 310)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuquesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Tel: 314 286 1800
Fax: 314 286 1810
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
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/dev_stage="4 weeks"
/lab_host="DH10B"
77 c 85 g 67 t
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/clone="1431017"
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/strain="C57BL/6J"
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72.5%;
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                                                                                                                                                                                                                                                                                            Score 149.8; 1
Pred. No. 1.2e
0; Mismatches
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nes 77;
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    255
                                     538 CCGAAATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCGGCCTACCTT 597
                                                                                                                                                                                                                                         435 GTGCAGCTGGTGCAGTCTGGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCC 376
                                                                                                                                                                                                                                                                              358 GIGCAGCIGCAGCAGICIGGGGIIGAGCIIGICCGAGGAGGGGCCIIAGICAAGIIGICC 417
                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                     GAACAGGGCCTGGAATGGATTGGATGCATTCATCCTGAGAATGGTAATACTGTATATGAC 537
CAGAAGTTTCAGGGCAGAGTCACCATGACCAGGGACACGTCCATCAGCACAGCCTACACG
                                                                                                                                                                                                  TGCAAAGCTTCTGACTTCAACATTAAAGACTATTATATCCACTGGGTGAAGCAGAGGCCT 477
                                                                              GGACAAGAGCTTGGGTGGATGGGACGGATCAACCCTAACAGTGGTGGCACAAACTATGCA 256
                                                                                                                                                          TGCAAGGCTTCTGGATACATCTTCACCGACTACTATATGCACTGGGTGCGACAGGCCCCT 316
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMAN); contains Alu repetitive element;, mRNA sequence AI201426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40UP from Gibco Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: prostate; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDS
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
/db_xref="taxon:9606"
/clone="TMACE:1943722"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B"
132 c 106 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ∕organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                        20.3%;
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                                                                                                                                                                                                                                                                                                                     Score 146.2; DB 3
Pred. No. 1.8e-35;
0; Mismatches 88
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Best Local Similarity
Matches 193; Conserv
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                                                                                                 TGCAAAGCTTCTGACTTCAACATTAAAGACTATTATATCCACTGGGTGAAGCAGAGGGCCT 477
                                                                                                                                                                          GTGCAGCTGCAGCAGTCTGGGGTTGAGCTTGTCCGAGGAGGGGCCTTAGTCAAGTTGTCC 417
                                                                         TGTAAGGCATCTGGATTCACCCTCACCAACTGCCATATGCACTGGGTGCGACAGGCCCCT
                                                                                                                                                  GTCCAACTGGTGCAGTCTGGGGGCTGAGGTGAAGAAGCCTGGGGGCCTCAGTGAAGCTTTCC 157
 GGGCAAGGGCTTGAGTGGGTGGGAATGATCAATTCTAGTGATGGTTATATAAAGTAACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 387)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 1722 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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AA569186
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similar to gb:L02325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pAMP10; mRNA made from liposarcoma, cDNA made by oligo-dT priming. Non- directionally cloned. Size-selected on agarose gel, average insert size 600 k Reference: Krizman et al. (1996) Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1061683"
/clone_lib="NCI_CGAP_Lip2"
/tissue_type="liposarcoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                               19.0%;
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_Lip2 Homo sapiens cDNA clone IMAGE:1061683
5 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);,
                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                               Score 136.6; DB 2
Pred. No. 1.7e-32;
                                                                                                                                                                                                                                                                                                                                            118 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston,R.
The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 294)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Mooris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1007196 294 bp mRNA EST 12-JUN-1998 ua73904.rl Soares 2NbMT Musculus cDNA colone 1363158 5' similar to gb.M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN); gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:896378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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AI007196
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                                                                                                      85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop:
                                                                                                                                                                                                                                                                         Soares and M.Fatima Bonaldo.
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                    /dev_stage="4 weeks"
/lab_host="DH10B"
68 c 77 g
                                                                                                                                                                                                                  /clone="1363158"
                                                                                                                                                           /tissue_type-"Thymus"
                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                  /clone_lib="Soares 2NbMT"
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18.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MO 63108
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Query Match Best Local Sim Matches 205;

Similarity 70.9 05; Conservative

Score 133.8; DB 28 Pred. No. 1.2e-31; 0; Mismatches 82;

DB 28;

Length

294; <u>ب</u>

Gaps

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RESULT
AA456778
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                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos Kucaba, T., Lacy, M., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA456778 400 bp mRNA EST zw27f11.rl Soares ovary tumor NbHOT Homo sapiens 5' similar to gb:X06764 IG KAPPA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMAN);, mRNA
AA456778
                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
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                                     /sex="Female"
/tissue_type="ovarian tumor"
                            /clone_lib="Soares ovary
                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitochondrial eukaryotes; Metazoa; Chordata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
                              tumor NbHOT'
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V-III REGION
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241 AGGTTCAGTGGCAGTGGGTCTGAGACAGÄCTTCACTCTCAACATCGGCAAGACTGGAGCC
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                                                                                   Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr.P.S.,
Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M.,
Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T.,
Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L.,
Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R.,
Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A.,
Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrie, A.,
Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M.,
Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H.,
Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C.,
Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A.,
Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of CDNA Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAGATGCTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTC
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Unpublished (1995)
Other_ESTs: THC24356
Contact: Venter, JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T27593 393 bp mRNA EST 06-SEP-1995 EST100653 Homo sapiens cDNA 5' end similar to immunoglobulin light chain, V region (GB:L01279) (HT:3043).
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Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; H
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Pred. No. 3.7e
0; Mismatches
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                      Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
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For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
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heria; Primates; Catarrhini; Hominidae;
   Gruber,J.,
,J., Li,H.,
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   Hudson, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raymond, I., Wei, Y.F., Man, Y.C., Rosen, C.A., Haseltlue, M.C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltlue, M.C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                AA710291
g2720209
                                                                                                                               vt53a04.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone 1166766 5' similar to gb:X02484_rnal IG KAPPA CHAIN PRECURSOR V-IV REGION (HUMAN); gb:J00560 mouse 1g kappa mrna from mopc21 6 other myeloma mrna 3' (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
For clone availability, additional sequence ar
information related to this EST, please check
Index (http://www.tigr.org/tdb/hg1/hg1.html)
Seq primer: M13 Reverse.
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 345)
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                                                  Mus musculus
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/db_xref="ATCC (1nhost):190766"
/db_xref="taxon:9606"
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/dev_stage="adult"
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                                                                                                                                                                                 TCACAGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATGTGCAGTCTGAAG
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                                                                                                    ACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTTTCCGTACACGTTCGGAGGGGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
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The WashU-HHMI Mouse EST Project
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h quality sequence stop: 140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained from 8 week old mouse. Colon was harvested 72 hours after irradiation with 1400 Gys. 1st strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adaptors [AATTCGGATCCTTG], digested with Not I and clinto the Not I and Eco RI sites of the modified pT7T3
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/lab_host="DH108"
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/db_xref="taxon:10090"
/clone="1166766"
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/strain="FVB/N"
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                                                                                              --CTGGTATCAGCAGAAGTCAAGCACCTCCCCCAAACTCTGGGTTTATGACACACATCCAAA 153
                                                                   CCAGGGGAAAGAGCCGCCCTCTCCTGCAGGGCCAGTCAGCGTGTTAGCAGCAGTCACTTA 101
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Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Euraryotae; Mammalia; Eutheria; Primates; Catarrhini; Ho
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
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Seg primer: M13 Reverse.
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                                                                                                                                                                                     Similarity
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/note="Organ: gall bladder; Vector:
Site_1: EcoRI; Site_2: XhoI"
/db_xrof="ATCC (1hhost):147008"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 TACCCATTCACGTTCGGCTCGGGGACAAAGTTGGAAATAAAAGGTTCT
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nugyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCACCTAGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACT
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                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96026280
Other_ESTs: THC168243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                               Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3018699056
              85
/note-"Organ: pancreas; Vector: pB
ECORI; Site_2: XhOI"
/db_xref="ATCC (inhost):190705"
/db_xref="taxon:9606"
/clone_lib-"Pancreas tumor I"
/dev_stage-"adult"
<1. .>370
5 a 107 c 94 g 77 t 7
                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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Rockville,
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           others
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REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
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Best Local Similarity
Matches 178; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 GATGCTGCCACTTATTATTGTTATCA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 TCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAAACCTGGC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weil, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pister, C.M. and Venter, J.C., Frastron, M. and Venter, J.C., France, M. and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGCAGCTGACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCACCATG
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   Email: arkerlav@tigr.org
For clone availability, addi
information related to this
                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                               Bioinformatics
                                                                                                                                                                                                                                                                                         Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                  Other_ESTs: THC87411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams, M.D., Kerlavage, A.R., Fleischmann, R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
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Pred. No. 1.5e-26;
0; Mismatches 85;
additional sequence and expression this EST, please check the TIGR Human
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162; Conserv
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zt44g02.rl Soares ovary tumor NbHOT Homo sapiens
5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                            1 (bases 1 to 379)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
Washdy-Merck EST project
Unpublished (1995)
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Seq primer: M13 Reverse.
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                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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Ecorl; Site_2: Xhol"
/db_xref="ATCC (inhost):192041"
/db_xref="taxon:9606"
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<1. .>333
85 c 80 g
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                                                                                                                                                                                                                                                                                                 ng69c07.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940044 similar to gb:M63438 IG KAPPA CHAIN PRECURSOR V-III REGION (HUMAN);, mRNA sequence.

AA515239
                                                                                                                   Unpublished (1997)
                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
                           Tissue Procurement: L. J
Emmert-Buck, M.D., Ph.D.
                                                                                        Contact: Robert Strausberg,
                                                                                                                                                                                                            Eukaryotae;
Vertebrata;
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                    g2254839
                                                            Email:
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cDNA Library Preparation: David B. Krizman, cDNA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                           (301) 496-1550
                                                          Robert_Strausberg@nih.gov
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/clone="725234"
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/lab_host="DH108 (ampicillin
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                                                                                        GGGACCAAGGTGGAAATCAAACGAACT 411
                                                                                                          GGGACAAAGTTGGAAATAAAAGGTTCT 321
                                                                                                                                                  GAAGATTCTGCAGTTTACTATTGTCAGCACTATGGTACCTCATTATGGACATTCGGCCAG
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High quality sequence stop: 413.
Location/Qualifiers
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/clone="IMAGE:940044"
/clone=11b="NCI_CGAP_Lip2"
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/lab_host="DH10B"
<1...>418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/note="Vector: pAMP10; mRNA made from liposarcoma, cDNA
made by Oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
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127 c
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is the number of results predicted by chance to have a ster than or equal to the score of the result being printed. Fived by analysis of the total score distribution.
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2274.252 Million cell updates/sec
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                                                                                                         Anti-human SC sing Coding sequence of Single chain bindi 18-2-3/TRY59 singl 18-2-3/TRY59. Sin Nucleic acid seque Nucleic acid seque Nucleic acid seque Pv(GP-4) immunosup Single chain anti-H22-anti-CEA antib Sequence encoding PLAP CC49/212 SCA CC49/212 SCA PLAP Sequence encoding Sequence encoding Sequence encoding Sequence encoding Sequence encoding Sequence symma heavence symma 
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Coding sequence of
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30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY I
KASPIZYA PG, King CR;
WPI: 94-025878/03.
P-PSDB; R44443.
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21-OCT-1992;
30-JUN-1992;
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Q55181;
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Example; Fig 8; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies not all (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell englineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. 1 animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 720 BP; 184 A; 178 C; 179 G; 179 T;
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                                   CAGCTGCAGCAGTCTGGGGTTGAGCTTGTCCGAGGAGGGGCCTTAGTCAAGTTGTCCTGC
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                                                                                                                  AAGTTGGAAATAAAAGGTTCTACCTCCGGATCTGGTAAATCTTCTGAAGGTAAAGGTGTG
                                                                                                                                                AAGTTGGAAATAAAAGGTTCTACCTCCGGATCTGGTAAATCTTCTGAAGGTAAAGGTGTG
                                                                                                                                                                                                                                  GCTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCGGGGACA
                                                                                                                                                                                                                                                                GCTGCCACTTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCGGGGACA
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Pred. No.
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                                                                                                                 Single chain antibodies specific for erbB-2 protein, gp185 - with labels or cytotoxin, useful for detection and treatment of tumour cells expressing this protein
Example 9; Columns 27-30; 28pp; English.

C The present cDNA sequence codes for a claimed single-chain antibody, chesignated e21(Fv), which binds to erbB-2. Monoclonal antibody e21

C was generated by immunising mice with N/erbB-2 cells overexpressing the gp185 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gp185 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours.
                                                   Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                 24-DEC-1996.

24-DEC-1996.

07-OCT-1991; US-772270.

07-OCT-1991; US-906555.

30-JUN-1992; US-96655.

14-MAY-1993; US-061092.

(ARON) ARONEX PHARM INC.

Bird RE, Kasprzyk PG, Ki.
WPI; 97-064831/06.

P-PSDB; W15186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1997 (first entry)
05-JUN-1997 (first entry)
Single-chain anti-erbB2 antibody e21(Fv) cDNA.
Single chain antibody; variable region; light chain; heavy chain;
Single chain antibody; variable region; light chain; heavy chain;
breast cancer; ovarian cancer; non-small cell lung carcinoma;
breast cancer; ovarian cancer; cytotoxic agent; erbB-2; ds.
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thes 0;
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RESULT 3
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PR 06-SEP-1994; US-408252.
PR 06-JUN-1995; US-468252.
PR 06-JUN-1995; US-468252.
PR 06-JUN-1995; US-468252.
PR 06-JUN-1995; US-468252.
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PR 06-SEP-1995; US-468252.
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PR 06-SEP-1995; US-468252.
PR 06-SEP-1995; US-468252.
PR 06-SEP-1996; US-468252.
PR 06-SEP-19

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libody; variable region; light chain; heavy ch

varian cancer; non-small cell lung carcinoma;

treatment; cytotoxic agent; erbB-2; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single chain antibodies specific for erbB-2 protein, gp185 - with labels or cytotoxin, useful for detection and treatment of tumour cells expressing this protein

Example 8; Columns 25-28; 28pp; English.

The present cDNA sequence codes for a claimed single-chain antibody, designated e23(FY), which binds to erbB-2. Monoclonal antibody e23 was generated by immunising mice with N/erbB-2 cells overexpressing the gp185 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PGR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gp185 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours.

Sequence 711 BP; 175 A; 182 C; 189 G; 164 T;
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07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061992.
(ARON-) ARONEX PHARM INC
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WPI; 97-064831/06.
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                                                                                                                                                                                                                                                   AGTTGGAAATAAAAGGTTCTACCTCCGGATCTGGTAAATCTTCTGAAGGTAAAAGGTGTGC
                                                                                                                                                                                                                                                                                                            CTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCCATTCACGTTCGGCTCGGGGACAA
AGTTCAAGGGCAAGGCCACATTTACTGTAGACAAGTCGTCCAGCACAGCCTACATGGAGC
               AATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCCGGCCTACCTTCAGC
                                                        AAGCTTCTGACTTCAACATTAAAGACTATTATATCCACTGGGTGAAGCAGAGGCCTGAAC
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                                                                       AGGGCCTGGAATGGATTGGATGGATTCATCCTGAGAATGGTAATACTGTATATGACCCGA
                                                                                                                  AGACTTCTGGTTACTCATTCACTGGCCACACCATGAACTGGGTGAAGCAGAGCCATGGAA
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Pred. No. 2.8e-106;
L; Mismatches 131;
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Best Loc
Matches
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21-APR-1994; 106257.
21-APR-1993; JP-094491.
07-MAR-1994; JP-036065.
(AJIN ) AJINOMOTO KK.
Hamura J, Kanayama Y, |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunosuppressant polypeptide - has ability to block interleukin-2 response Claim 17; Page 29; 37pp; English.

MAb capable of binding to the gamma chain of the IL-2 receptor, and thus of blocking the IL-2 response, is produced by mouse hybridoma line GP-2 (FERM BP-4641). DNA encoding the variable region of this MAb was expressed in E. coli, yielding Fv(GP-2) with immumosuppressive activity.

Sequence 732 BP; 180 A; 204 C; 182 G; 166 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q73678 standard; DN/
Q73678;
Q9-MAY-1995 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
EP-621338-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAD; monoclonal antibody; hybratic hybr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fv(GP-2) immunosuppressive
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                         TTGTCCTGCAAAGCTTCTGACTTCAACATTAAAGACTATTATATATCCACTGGGTGAAGCAG
                                                                                                                                                                           GGGACAAAGTTGGAAATAAAAGGTTCTA---CCTCCGGATCTGGTAAATCTTCTGAAGGT
                                                                                                                                                                                                                                                                                                               GAAGATGCTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCG
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TIGTCCTGCAAGGCTTCTGGCTACACATTCACCAGCTACTGGATGCACTGGGTGAAGCAG
                                                                                   ACGCAGGTCAAACTCGAGGAGTCTGGATCTGAGCTGGTGAGGCCTGGAGCTTCAGTGAAG
                                                                                                                             AAAGGTGTGCAGCTGCAGCAGTCTGGGGGTTGAGCTTGTCCGAGGAGGGGGCCTTAGTCAAG
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lon; GP-2; Fv(GP-2);
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Best Local S
Matches 509
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30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY I
KASPIZYK PG, King CR;
WPI; 94-025878/03.
P-PSDB; R45442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9400136-A.
06-JAN-1994.
21-OCT-1992;
30-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Fig 7; 37pp; English.

Example; Fig 7; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies r 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. animals given a combination of the 2 Abs, tumours completely regressed after 11 days.

Sequence 711 BP; 175 A; 183 C; 187 G; 165 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
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Synthetic.
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c Local L
509;
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                                                                                                                                                               CCTGCAGTGCCAGCTCAAGTGTAAGTAACATGCACTGGTATCAGCAGAAGTCAAGCACCT 121
                                                                                                                                                                                                                                                           TGCAGCTGACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCACCATGA 61
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                                                                                                                                                                                                                                   TGCAGCTGACCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACAATGA
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                                                                                                                                         CTTGCAGGGCCACCCCAAGTGTAAGTTACATGCACTGGTATCAGCAGAAGCCAGGATCCT 127
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                                                                                                                                                                                                                                                                                                                               Similarity 79.:
09; Conservative
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2e-105;
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target cells
Disclosure; Fig 3; 26pp; English.

Disclosure; Fig 3; 26pp; English.

The sequence is an NdeI-HindIII fragment encoding the L and H chains of murine MAD OVB3, joined together via a linker. The sequence is present in clone powB3158-1 in which the 3' end is linked to the 5' end of the coding sequence for PE40, a a Pseudomonas exotoxin lacking domain I. The protein expressed by the clone can be used to kill specific target cells.

Commence 738 BP; 181 A; 193 C; 192 G; 172 T;
                                                                                                                                                                                                                                                                                                                                                                                                             US7463111-A.
28-MAY-1991.
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Key
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Q12405;
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OVB3 light and heavy chains.
Immunoglobulin; immunotoxin;
                                                                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                                                                                Rapid cloning of antibody
by fusing genes with DNA e
target cells
                                                                                                                                                                                                                                                                                    P-PSDB; R12798.
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11-JAN-1990; US-463111.
(USSH ) NAT INST OF HEALTH.
Pastan I;
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Best Loca
Matches
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15-FEB-1996; 027622.
15-FEB-1996; JF-0270
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  Producing single chain Fv antiborant expression in an inclusion body co-expression with a chaperonin
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le chain Fv; scFv; antibody; E. coli; anti-T:
-gpl30 antibody; inclusion body; chaperonin;
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Pred. No. 1.1e
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Best Local S
Matches 522
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The sequences given in T91614-15 encode single chain Fv (scFv) antibodies which are produced in E. coli. The scFv's are derived from an anti-T3 antibody or an anti-T9130 antibody and are produced either by: (1) expression as an inclusion body, followed by folding (i.e. by denaturation and solubilisation) or (2) expression as a soluble fraction by co-expression with chaperonin. Using the methods, scFv can be produced in E. coli, either in a soluble fraction or in inclusion bodies. Like the parent double chain antibodies, the scFv polypeptides are useful in immunological diagnosis or for separation and purification, but they lessen the side effects caused by antibody constant regions. The availability of scFv polypeptides contributes to fundamental research and development of diagnostic and therapeutic
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REŞULT 9 T91614 . ID T91614

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Best Local
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22-DEC-1997 (first entry)
cDNA encoding an anti-T3 antibody deriv
Single chain Fv; scFv; antibody; E. col
anti-gp130 antibody; inclusion body; cl
Synthetic.
Key
Location/Qualifiers
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                                              TCCGAGGTCAAGCTGCAGGAGTCTGGGGGGAGGCTTAGTGAAGCTTGGCGGGTCCCTGAAA
                                                                                                       GGGACAAAGTTGGAAATAAAAGGTTCTACCTCCGGATCTGGTAAATCTTCTGAAGGTAAA
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                                                             -GGTGTGCAGCTGCAGCAGTCTGGGGGTTGAGCTTGTCCGAGGAGGGGCCTTAGTCAAG
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/note= "No stop o
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pos:385. .387,
p codon given"
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1.5e-78;
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anti-T3 antibody;
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                                                                                                                                   Fig. 1. Single chain poly:peptide for binding antigen - comprising light provided that the provided linker provided by peptide linker provided by Figure 39; 78pp; English.

Example 9; Figure 39; 78pp; English.

The single chain polypeptide is derived from the mature light and comprises a first provided provi
                                      Query Ma
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02-SEP-1986; US-902971.
02-SEP-1987; US-902110.
19-JAN-1989; US-299617.
25-APR-1990; US-512910.
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CAAAGCTTCTGACTTCAACATTAAAGACTATTATATCCACTGGGTGAAGCAGAGGCCTGA
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RESULT T13739 US5534621-A.
09-JUL-1996.
02-SEP-1986;
02-SEP-1986;
02-SEP-1987;
19-JAN-1989; T13739; Single chain binding molecule 18-2-3/TRY202' DNA. Antibody engineering; single polypeptide chain binding single chain antibody; SCR; heavy chain; light chain; monoclonal antibody; MAD; immunoaffinity purification; Key Chimeric 11-0CT-1996 18-2-3/TRY202'; ss. 11 standard; Mus synthetic. 902971. US-902971. US-092110. US-299617. sp; Location/Qualifiers 619. .621 /transl\_except= 658. .660 /transl\_except= /\*tag= DNA; /\*tag= entry) 720 ø ВP (658. (619. aa:Ile)

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Example 9; Fig 39; 78pp; English.

A DNA construct (713739) codes for single chain binding molecule ill-2-3/TRY202/2 (R99649), in which VL and VH regions of anti-cliner composed primarily of alternating Gly and Ser residues, with illner composed primarily of alternating Gly and Ser residues, with expressed in E.coli. Soluble, folded chain antibody (SCA) was expressed in E.coli. Soluble, folded chain antibody (SCA) was obtd. which was capable of exhibiting a biological binding activity equivalent in specificity and affinity to that of a monoclonal antibody. The SCA has the advantages of smaller size, greater stability and reduced cost.

Sequence 720 BP; 180 A; 184 C; 175 G; 181 T;
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01-APR-1993; US-040440
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RE, Hardman K,
96-333309/33.
                                                                                                                                                                                                                                                                                                                                                                                                        CAAGCTTGAGCTGGAAGGTAAATCTTCTGGTTCTGG-----TTCCGAATCTAAATCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTGGCAGTGGGTCTGGAAACTCTTACTCTCACGATCAGCAGCAGCATGGAGGCTGAAGA
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*NATGAACAGTCTGCAAAATGATGACACAGCCATATACTACTGCGCAAACGACTGGAACG
                    GCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTACTGTGCTTCTTATTACTACTACTA
                                                                                                      GAAATTCCAGGGCAAGGCCAGTATAACAGCAGAGAGATCCTCCAACGCGGCCTACCTTCA
                                                                                                                                                                                                                                          CACTGTCTCTGGGTTTTCATTAACCAACTATGGTGTACACTGGGTTCGCCAGCCTCCAGG
                                                                                                                                                                                                                                                                                CAAAGCTTCTGACTTCAACATTAAAGACTATTATATCCACTGGGTGAAGCAGAGGCCTGA
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                                                                                                                                                             AAAGGGTCTGGAGTGGCTGGGAGTAATATGGGCTGG---TGGAAACACAAATTATAATTC
                                                                                                                                                                                                     ACAGGGCCTGGAATGGATTGGATGGATTCATCCTGAGAATGGTAATACTGTATATGACCC
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                                                                               AGCTCTCATGTCCAGACTGAGCATCAGCAAAGACAATTCCAAGAGCCAAGTTTTCTTAAA
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Pred. No. 8e-77;
0; Mismatches 210
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Best Local S
Matches 493
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21-MAY-1996;
02-SEP-1986; US-902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-299617.
25-APR-1990; US-512910.
01-APR-1990; US-51200.
06-JUN-1995; US-468988.
(ENZO-) ENZON LABS INC.
                                                                                                                                                                                                                                                                                                                                for labelled or immobilised antibody, are less immunogenic, easis to engineer, more stable and less expensive Example 9; Fig 39A-B; 78pp; English.

Computer-designed construct 18-2-3/TRX202' (W02191), encoded by the DNA sequence given in T36463, comprises the variable regions of the light and heavy chains of anti-fluorescein monoclonal antibody (Mab) 18-2-3 linked by a peptide designed to fit into a groove on the backside of the variable domain structure. The 18-2-3 VH and VL regions were obtd. by PCR amplification of hybridoma RNA, and the DNA construct was inserted into vector pGX3703 and introduced into E. coil. 18-2-3/TRX202' was expressed as a single chain molecule. It exhibited biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-2-3/TRY202' single chain binding protein-encoding Antibody engineering; monoclonal antibody; MAb; single chain antibody; immunoassay; fluorescein; 18-2 single chain binding protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ENZO-) ENZON LABS I:
Bird RE, Hardman K,
WPI; 96-259060/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric Mus musculus;
Chimeric synthetic.
Key Locatics
cds 658.
                                                                                                                                                                                                                                                                                             binding activity equivalent in specifically and that of the original MAb.
Sequence 720 BP; 180 A; 184 C; 175 G.
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                                                                                        CTCCCCCAAACTCTGGGTTTATGACACATCCAAACTGGCTTCTGGAGTCCCAGGTCGCTT
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                                                                                                                                                                                           GCTGACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCACCATGACCTG
TGCTGCCACTTATTATTGTTATCAGGGGAGTGGGTACCCATTCACGTTCGGCTCGGGGAC
                                                                                                                             CAGGGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTACCAGCAGAAGTCAGGTGC
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02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-299617.
(GENE-) GENEX CORP.
Ladner RC, Bird RE, Hardman KWPI; 90-260350/34.
                                                                                                                                                                                                               See also
Sequence
                                                                                                                                                                                                                              The sequence was constructed from the variable regions of an antifluorescein MAb, 18-3-2, an IgM. The VL and VH cDNA sequences were synthesised by priming on RNA isolated from hybridoma cells. The sequence encodes a single chain binding molecule comprising the variable regions of heavy and light chains linked by peptides. The peptide linker was computer-designed to fit inyo a groove on the backside of the variable domain structure and is composed primarly of alternating Gly and Ser residues. Glu and Lys residues are included to enhance solubility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R06482.
Single polypeptide chain bir
variable region of antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variable region.
Disclosure; Fig 39; 68pp;
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Q05714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody;
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GCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAAAAGGTCAACATGACCTG
                                                                                           al Similarity 68. 492; Conservative
                                                                                                                                                                                                               Q05708-Q05719.
724 BP; 180
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CC The single chain polypeptide is derived from the mature light and CC the single chain polypeptide is derived from the mature light and CC the single chain polypeptide is derived from the mature light and CC the single chain of a mouse monoclonal antibody (MAb) and has affinity CC chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the light CC chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the heavy chain variable CC region of an antibody and at least one peptide linker linking the CC first and second polypeptide chains. The resulting single chain CC (in vivo and in vitro), imaging, purifications and biosensors. CC This particular single chain binding molecule was designated TRY59 CC and contains one linker peptide.

SQ Sequence 741 BP; 172 A; 188 C; 192 G; 189 T;
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Best Local Similarity
Matches 504; Conser
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09-NOV-1993.
02-SEP-1986; 902971.
02-SEP-1986; US-902971.
02-SEP-1989; US-092110.
19-JAN-1989; US-295617.
25-APR-1990; US-512910.
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Bird R., Hardman K, Ladner
WPI: 93-367875/46.
P-PSDB; R43677.
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                              CCCGAAATTCCAGGGCAAGGCCAGTATAACAGCAGACACATCCTCCAACGCGGCCTACCT
                                                                                                                          CTGTGCAGCCTCTGGATTCACTTTCATTAGCTATGGCATGTCTTGGGTTCGCCGAACTCC
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pr Immuno:purificn. using single binding chain molecule including practices antigen binding parts of antibody light and heavy chain variable presents connected by a linker is smaller, stabler and less present than complete antibodies

Presentive than complete antibodies

Example 3; Fig 28; 78pp; English.

A DNA construct (T13737) codes for single chain binding molecule TRY59 (R99647), in which amino acids (aa) 1-105 of the VL region of anti-bovine growth hormone mouse IgG1 monoclonal antibody 3C2 and aa2-123 of the 3C2 VH are joined by a peptide linker from the CC and aa2-123 of the 3C2 VH are joined by a peptide linker from the CC region of the IgA anti-phosphorylcholine myeloma antibody MCPC-603. The construct was expressed in E.coli. Single chain binding adjected to the security of the heavy and light chain capuregate variable region of the native antibody but have the advantages of smaller size, greater stability and reduced cost.

So Sequence 741 BP; 172 A; 188 C; 192 G; 189 T;
                                                                                                                                                                                                                                                           US5534621-A.
09-JUL-1996.
02-SEP-1986;
02-SEP-1987;
02-SEP-1987;
19-JAN-1989;
25-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-1996 (first entry)
Single chain binding molecule TRY59 DNA.
Antibody engineering; single polypeptide chain binding molecule;
heavy chain; light chain; monoclonal antibody; MAD;
bovine growth hormone; bGH; immunoaffinity purification; TRY59; in the chimeric Mus. Sp.;
                                                                                                                                                                                    Bird RE, Hardman K, Ladner WPI; 96-333309/33. P-PSDB; R99647.
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06-JUN-1995;
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US-902971.

US-092110.

US-299617.

US-512910.

US-612910.

US-468992.
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Query Match Best Local Sim Matches 504;

Similarity

44.6%; ilarity 69.0%; Conservative

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Score 321.2; Pred. No. 1.3e 0; Mismatches

3e-76; DB 1;

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Search completed: May 13, Job time: 1188 sec 1999, 09:55:30

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd
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OM protein protein search, using sw model

Run

May 13, 1999, 09:40:48; Search time 21.53 Seconds (without alignments) 412:360 Million cell up

cell updates/sec

Perfect score: US-08-704-178-3 1267

Sequence: 1 MDLQLTQSPAILSASPGEKV.....RRVTDWYFDVWGAGTTVTVS

Scoring table: BLOSUM62

116738 seqs, 37460341 residues

Database Searched:

PIR\_58:\*

4 3 2 L pir2:\*
pir3:\*
pir4:\* pir1:\*

Pred. No. d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

## RESULT PC4402

hapten-specific single-chain antibody variable fragment and alkaline phosphatase C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 03-Sep-1998 #sequence\_revision 03-Sep-1998 #text\_change 03-Sep-1998 C;Accession: PC4402 C;Accession: PC4402 R;Suzuki, C:; Ueda, H:; Suzuki, E:; Nagamune, T. J. Biochem. 122, 322-329, 1997 J. Biochem. 122, 322-329, 1997

A; Reference number: PC44 A; Accession: PC4402 A; Status: preliminary A; Residues: 1-287 <SUZ> A; Title: Construction, bacterial expression, and characterization of hapten-specific A; Reference number: PC4402

Query Match 48.6 Best Local Similarity 51.0 Matches 132; Conservative 48.68; 32; Score 615.5; DB 3; Pred. No. 3.5e-38; Length 287; Indels 25; Gaps 6;

밁 ş 23 MDIQAVVTQESA-LTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNR 81 1 MDLQ--LTQSPAILSASPGEKVTMTCR----ATPSVSYMHWYQQKPGSSPKPWIYTTSNL 54

밁 Š 82 55 ASGVPARFSGGGSGTSYSLTYSRYEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSG 114 APGVPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLSSADDAK 141

ğ В 142 KDDAKKDDAKKDGQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPG 115 KSSEGKG------VQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHG 162 201

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Вþ 202 163 KNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTD 222 RGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR--YD 259

δÃ 밁 260 YYGSSYFDYWGQGTTLTVS 278 223 W----YFDVWGAGTTVTVS 237

PH0887

Ig heavy chain V region (anti-CD3) - mouse (fragment)

Ig heavy chain V region (anti-CD3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Patte: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 16-Aug-1996

C;Accession: PH0887

C;Accession: PH0887

R.Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldma J. Exp. Med. 175, 217-225, 1992

A;Title: Development of humanized bispecific antibodies reactive with cytotoxic lymph A;Reference number: PH0885; MUID:92113462

A;Accession: PH0887

A;Molecule type: mRNA
A;Residues: 1-122 <SHA>
A;Note: the authors translated the codon TTC for residue 70 as Leu C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin

Query Match Best Local Similarity Matches 102; Conserv Conservative 42.6%; Score 540; DB 2; Pred. No. 4.2e-33; 6; Mismatches 8 Length 122; Indels 4.

Gaps

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Ig heavy chain V region (MOPC 104E) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 16-Aug-1996
C:Accession: A02039
R:Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, I Biochemistry 21, 5415-5424, 1982
A:Title: Complete amino acid sequence of a mouse mu chain: homology among heavy A; Reference number: A02039; MUID:83075344
A; Accession: A02039
A; Molecule type: protein
A; Residues: 1-117 <KEH>
C:Comment: The 91ycosylated asparagine residue does not have the usual N-X-S/T C:Comment: This protein binds dextran.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM'>
F:22-96/Disulfide bonds: #status predicted
F:55/Binding site: carbohydrate (Asn) (covalent) #status atypical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (129) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-199
C:Accession: 137267
R;Rfff-Jamison, S; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and 11ght chain variable region sequences and antibody prop
A;Reference number: A38740; MUID:91177923
A;Cession: 137267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
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Best Local S
Matches 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGLTTVVAKSYYFDYWGQGTTL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARR-----VTDWYFDVWGAGTTV 234
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95;
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95; Conservative
                                                                       Similarity
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                                                       Conservative
                                                                       39.2%;
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Pred. No. 5.2e-30;
0; Mismatches 12
                                                     Score 496.5; DB
Pred. No. 6e-30;
9; Mismatches
                                                                                      DB 1;
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                                                       Indels
                                                                                        Length 117;
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RESULT
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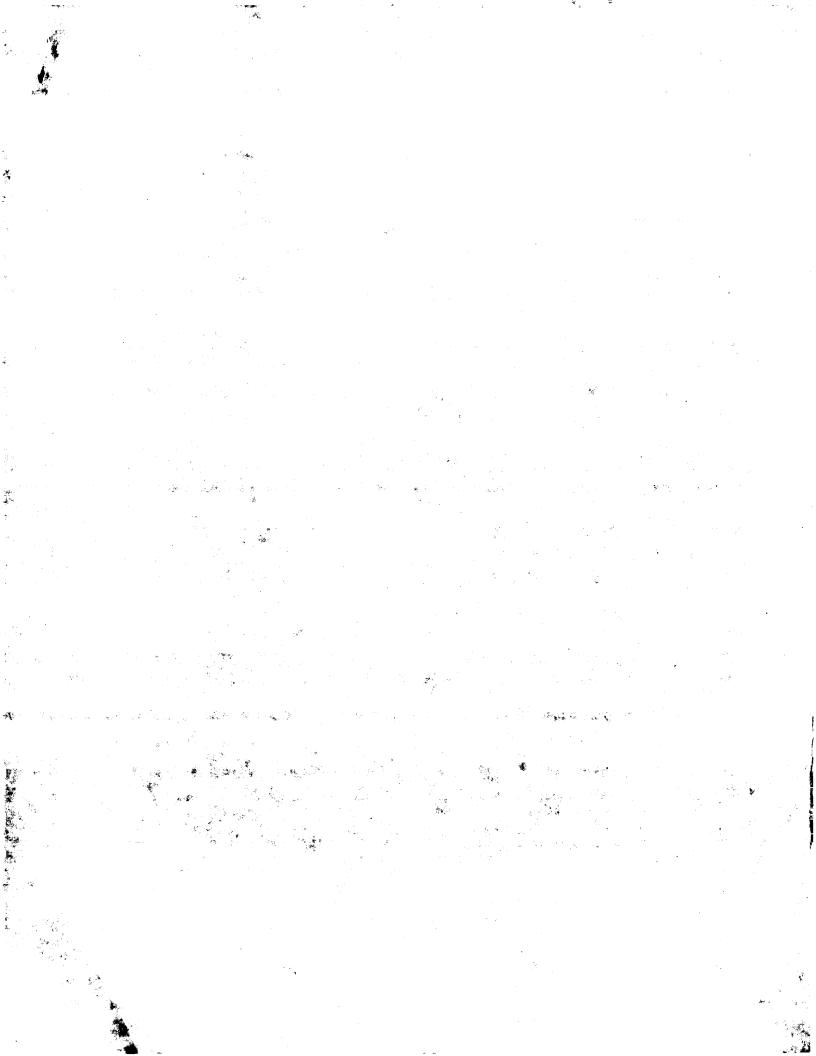
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Ig heavy chain V region (Py69) - mouse
C; Species: Mus musculus (house mouse)
C; Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-/
C; Accession: C37267
R; Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A; Title: Heavy and light chain variable region sequences and antibod A; Reference number: A38740; MUID:91177923
A; A; Accession: C37267
A; Status: preliminary; not compared with conceptual translation A; Molecule type: mRNA
A; Residues: 1-128 <RUF>
C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                  anti-AFP antibody F3 light chain variable region - mov C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1997 *sequence_revision 23-Jan-1998 *te C:Accession: PC4405
R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese BioChem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library of the A; Reference number: PC4405
A;Accession: PC4405
A;Accession: PC4405
A;Experimental source: spleen cell
C:Superfamily: immunoglobulin V region; immunoglobulin
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PC4405
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                    FSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK 107
                                                                                                 DLQLTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPAR 61
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FSGSGSGTSYSLTISRVEAEDAATYYCQQWRDNPPTFGGGTKLEIK
                                                                             DIELTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSPKRWIYDTSKLASGVPAR
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Pred. No. 8.5e-30;
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No. 1.6e-29;
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A; Molecule type: protein
A; Residues: 1-117 <5CH>
A; Residues: 1-117 <5CH>
A; Note: the sequences of 10 hybridoma proteins that als
C; Comment: This protein binds dextran.
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; hybridoma; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
F; 22-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Status: preliminary; not compared with conceptual A;Molecule type: nucleic acid
A;Residues: 1-120 <SIM>
A;Residues: 1-120 <SIM>
C;Superfamily: immunoglobulin V region; immunoglobul C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that di A;Reference number: A45722; MUID:93100833
A;Accession: E45722
Ig kappa chain V region (2D3) - mouse C;Species: Mus musculus (house mouse) C;Date: 07-Jun-1990 #sequence_revision C;Accession: PLOU82 R;Meek, K.; Hasemann, C.; Pollok, B.; J. Exp. Med. 169, 519-533, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Amino acid sequence A;Reference number: A26242; NA;Accession: A26242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Schilling, J.; Cl
Nature 283, 35-40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g heavy chain V region (J558) - mouse Species: Mus musculus (house mouse) Date: 30-2un-1991 #sequence_revision accession: A26242
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                                                                                                                                                                                                                                                                                                                                 . Similarity
93; Conser
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Pred. No. 1.8e-29;
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Pred. No. 2.7e-29;
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                      Alkan,
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A;Experimental source: strain BALB/c
A;Note: the sequence shown here is from the V kappa region of C;Superfamily: immunoglobulin V region; immunoglobulin homolog C;Keywords: heterotetramer; immunoglobulin
R.Simpson, J.A.; Chow, J.C.; Baker, J.; Avda J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies A;Reference number: A45722; MUID:93100833
A;Accession: F45722
A;Status: preliminary; not compared with con A;Molecule type: nucleic acid
A;Residues: 1-120 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-137 <KOF>
A; Cross-references: GB:M20831; NID:g196949; PID:g196950
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain precursor V region (BXW16) - C;Species: Mus musculus (house mouse) C;Date: 21-May-1990 #sequence_revision 31-De
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H32513
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A; Residues: 1-106 <MEE>
                                                                                                                         anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-May-19C;Accession: F45722
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A; Title: Immunoglobulin kappa light chain
A; Reference number: A94689; MUID:88331394
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Pred. No. 6.1e-29;
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                                                                               A;Cross-references: GB:D00307; NID:g220448; PID:d1000661; PID:g220449
A;Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly C;Comment: The gene encoding this protein was isolated from a hybridoma that produces an C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG> F;20-135/Product: Ig heavy chain V region PAR #status predicted <
                                                                                                                                                                                                                                                    C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_cha C;Accession: PS0057
R;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T. J. Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families A;Reference number: PS0057; MUID:89197817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X59172
C;Superfamily: immunoglobulin V region; im
C;Keywords: heterotetramer; immunoglobulin
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C:Species: Mus musculus (house mouse)
C:Decte: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C:Accession: S26319
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: sequence extracted from NCBI backbone (NCBIP:120594) C; Superfamily: immunoglobulin V region; immunoglobulin homol C; Keywords: glycoprotein
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A; Residues: 1-135 < YAO>
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A; Residues: 1-114 <STA>
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C; Species: Mus musculus (house mouse)
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Pred. No. 2.1e-28;
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Ig heavy chain V region (A52) - mouse C;Species: Mus musculus (house mouse) C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 16-Aug-1996 C;Accession: F30502 R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988 A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZI A;Reference number: A30502; MUID:88315787 A;Accession: F30502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (anti-cyclosporin F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 *sequence_revision 15-Jan-1993 *text_change 16-Aug-1996
C;Accession: PH0099
R;Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniau
Mol. Immunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to c;
A;Reference number: PH0087; MUID:91042649
A;Accession: PH0099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                              C;Superfamily: immunoglobulin V region; im
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-119 <EIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: immunoglobulin V region; immu C; Keywords: heterotetramer; immunoglobulin F; 31-35/Region: complementarity-determining F; 50-66/Region: complementarity-determining
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A; Residues: 1-119 <SCH>
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Pred. No. 3.1e-28;
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Pred. No. 2.9
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27.2 27.1

109 ب ب

KV3B\_HUMAN

P01620 homo sapien P01669 mus musculu

ALIGNMENTS

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein protein search, using sw model

Run May 13, 1999, 09:55:33; Search time 16.53 Seconds (without alignments).
384.825 Million cell updates/sec

Perfect score:

Sequence: US-08-704-178-3
1267
1 MDLQLTQSPAILSASPGEKV.....RRVTDWYFDVWGAGTTVTVS 237

Scoring table: BLOSUM62

Searched: 74019 segs, 26840295 residues

Database : SwissProt\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

40 41 42 43	33333333333333333333333333333333333333	331 331 331 331	10000000000000000000000000000000000000	Result
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AN SEQUENCE.

AN MEDLINE; 80078170.

AN MEDLINE; 80078170.

RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;

RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;

RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;

RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;

RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;

RA NATURE 283,254-0(1980).

CC -1- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS, MANY OF WHICH OCCUR IN COUNTY THE D AND J SEGMENTS.

CC -1- THIS PROTEIN BINDS DEXTRAN.

DR HSSP, PO1789; 2FGW.

KW IMMUNOSLOBULIN V REGION.

FT DISULFID 22 96 BY SIMILARITY.

TY13\_MOUSE

TY13\_MOUSE

TANDARD;

PRT; 117 AA.

PRT; 121-JUL-1986 (REL. 01, CREATED)

TY 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

TY 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)

E IG HEAVY CHAIN V REGION (J558).

S MUS MUSCULUS (MOUSE).

C EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

C EUTHERIA; RODENTIA.

R 111

R 121

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DP QA	Ma B Q	SOFF	E X	DR DR	នន	32	<b>2</b> 3	2 2 2	R R	88	20	E c	ijij	DJ A	RESULT HV12_M
122 VQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYN 181     :    :     : :     :  :  :  :  :  :	Query Match Best Local Similarity 81.0%; Pred. No. 5.6e-31; Matches 94; Conservative 9; Mismatches 12; Indels 1; Gaps 1;	}	IMMUNOGLOBULIN V REGION; GLYCOPROTEIN. DISULFID 22 96 BY SIMILARITY.	PIR; A02039; MHMS4E. HSSP; P01772; 1FGV.	ALSO BEEN DETERMINED!- THIS PROTEIN BINDS DEXTRAN.	-i- THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS	HOOD L.E.;	B STUDNIN T C CONTITUD TO BOCKER T	SPOTENCE:	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	MUS MUSCULUS (MOUSE).	IG HEAVY CHAIN V REGION (MOPC 104E).	(REL. 01,	6 (REL.	LT 1 MOUSE HY12_MOUSE STANDARD; PRT; 117 AA.
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REGION

Indels Length

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/51_MOUSE

D HV51_MOUSE

C P06330;

DT 01-JAN-1988 (REL. 06, CREATED)

DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE

DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE

DE IG HEAVY CHAIN V REGION (AC38 205.12).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA

OTHERIA; RODENTIA.
RESULT HV15_MOUSE
ID HV15_M
AC P01759
AC P01759
DT 21-JUL
DT 21-JUL
DT 21-FEB
DE IG HEAR
OS MUS MU
OC EUTHER
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Matches 93
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Best Local Similarity
Matches 91; Conser
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DILDROP R., BOVENS J., SI
TMRO J. 3:517-523(1984).
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SEQUENCE
                                                                          HV15_MOUSE STANDARD; PRT; 1
p01759;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UP
01-FEB-1991 (REL. 17, LAST ANNOTATION |
1G HEAVY CHAIN PRECURSOR V REGION (BCL
 SEQUENCE FROM N.A.
MEDLINE; 82222262.
KNAPP M.R., LIU C.-P.,
BLATTNER F.R.;
                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                HSSP;
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; P01772; 1FGV.
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Matches 84
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EMBL; J00494; G195011; -.
PIR; A02042; HVMSB1.
HSSP; P01789; 1JEL.
HMMUNOGLOBULIN V REGION; S
SIGNAL 1 19
CHAIN 20 136
NON_TER 136 136
SEQUENCE 136 AA; 15078
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE: 83.71.467.
KAARTINEN M., GRIFFITHS G.M.,
NATURE 304:320-324(1983).
-!- FUNCTION: ANTI-7-PHENYL O
EMBL; K007735; G196435; -.
HSSP; P01679; 1FVB.
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   P04940;
13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
11-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-VI REGION (NQ2-17.4.1).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KV6F_MOUSE
                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA;
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                                                        LTQSPAILSASPGEKYTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPARFSG 64
                                                                                              QKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCARYYGN-YFDYWGQGTTLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYFDVWGAGTTVTVS
                                                                                                                                      80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               RODENTIA.
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1 23
3 34
4 48
19 55
66 87
96 96
97 106
          STANDARD;
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                                                                                                                                                 34.58;
77.78;
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                                                                                                                                                                                                                                                                                        HYBRIDOMA
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                                                                                                                                                                                        ME;
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                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                    OXAZOLONE
                                                                                                                                     Score 437; DB
Pred. No. 1.4e
L1; Mismatches
                                                                                                                                                                                                          FRAMEWORK
BY SIMILAR
                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING FRAMEWORK 2.
COMPLEMENTARITY - DETERMINING FRAMEWORK 3.
COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 439.5;
Pred. No. 1.
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          PRT;
                                                                                                                                                                                                                                                                                                                                        MARKHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                    (PHOX)
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ACCOMPAND DEFINE TO SERVING SE
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KV6G_MOUSE
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Best Local S
Matches 79
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KAARTINEN M., GRIFFITHS G.M.,
NATURE 304:320-324(1983).
-!- FUNCTION: ANTI-2-PHENYL O:
EMBL; K00740; G196445; -.
                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (REL. 05,
13-AUG-1987 (REL. 05,
13-AUG-1987 (REL. 27,
01-OCT-1993 (REL. 27,
1G KAPPA CHAIN V-VI RE
MUS MUSCULUS (MUUSE).
EUKARYOTA; METAZOA; CH
       DOMAIN
DISULFID
NON_TER
SEQUENCE
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DOMAIN
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DOMAIN
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DOMAIN
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13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
01-OKT AND AUGUST (REGION (NG6-8.3.1).
IG KAPPA CHAIN V-VI REGION (NG6-8.3.1).
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETTERMATETA
                                                                              DOMAIN
DOMAIN
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                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                     KAARTINEN M., GRIFFITHS G.M., NATURE 304:320-324(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KV6G_MOUSE
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                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 83271467.
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                                                                                                                                                                                      IMMUNOGLOBULIN
                                                                                                                                                                                                    !- FUNCTION: ANTI-2-PHE
MBL; K00737; G196439; -
SSP; P01679; 1FVB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGXPARFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPARFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01679;
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05, LAST SEQUENCE UPDATE)
27, LAST ANNOTATION UPDATE)
VI REGION (NQ2-48.2.2).
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         MW;
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Pred.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.

BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
                                         COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                               COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
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COMPLEMENTARITY-DETERMINING
                                                                                            FRAMEWORK 3.
                                                                                                               COMPLEMENTARITY - DETERMINING
                                                                                                                                                                  FRAMEWORK 1.
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         1AB8295D CRC32
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3.
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                                                                                                                                                                                                                                     (PHOX) ANTIBODY
                                                                                                                                                                                                                                                                        A.F.,
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.3e-26;
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RESULT 8
KV6H_MOUSE
                    P04944;
P04944;
13-AUG-1987 (REL. 05, LAST SEQ
f 13-AUG-1987 (REL. 27, LAST AN)
T 01-CCT-1993 (REL. 27, LAST AN)
DE IG KAPPA CHAIN V-VI REGION (N
OS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA
PHTHERIA; RODENTIA.
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Best Local S
Matches 79
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Best Local
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DISULFID
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SEQUENCE
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DOMAIN
DOMAIN
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KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN (NATURE 304:320-324(1983).

-I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY EMBL; K00739; G196443; -.

HSSP; P01679; IFVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDA:
01-OCT-1993 (REL. 27, LAST ANNOTATION UPI
IG KAPPA CHAIN V-VI REGION (NQ5-61.1.2).
                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
         SEQUENCE FROM N.A. MEDLINE; 83271467.
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KAARTINEN M.,
                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOGLOBULIN
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                                                                                                                                                                       GGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK
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                                                                                                                MOUSE
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GRIFFITHS
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                                                                                                                STANDARD;
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                                                                        . 05, CREATED)
. 05, LAST SEQUENCE ANNI
                                               CHORDATA;
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76.7%;
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76.7%;
G.M.,
                                                                                                                                                                                                                                                                                                                                                                                   HYBRIDOMA
                                                                                                                                                                                                                                                                                     MW;
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                                                                SEQUENCE UPDATE)
ANNOTATION UPDATE)
(NQ5-78.2.6).
                                                                                                                                                                                                                                              Score 431; DB 1
Pred. No. 4e-26;
                                                                                                                                                                                                                                                                                                                                           FRAMEWORK 1.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 431;
Pred. No.
                                                                                                                                                                                                                                                                                                       FRAMEWORK 3.

COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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MARKHAM A.F.,
                                               VERTEBRATA;
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                                               TETRAPODA;
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MILSTEIN C.;
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                                               MAMMALIA;
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Best Local S
Matches 81
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Best Local S
Matches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE: 83771467.

KAARTINEN M., GRIFFITHS G
NATURE 304:320-324(1983).

EMBL; K00746; G554059; -.

HSSP; P01679; 1BAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
NON_TER
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UP
01-OCT-1993 (REL. 27, LAST ANNOTATION
1G KAPPA CHAIN V-VI REGION (NQ2-6.1).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMUNOGLOBULIN
64
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FUNCTION: ANTI-2-PHEN
L; K00744; G196453; -.
P; P01679; 1FVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK 107
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                           GGSGTSYSLTVSRVEAEDAATYYCQQWSRSPP--TFGGGSKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                          Similarity 77.1
31; Conservative
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11611 MW;
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11713
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77.1%;
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                                                                                                                                                                                                                                                                                                                , WM
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                                                                                                                                                                                       Score 429; DF Pred. No. 5.76
                                                                                                                                                                                                                                                                                                                                                           CONFLEMENTARITY - DETERMINING 1
FRAMEWORK 2.
CONFLEMENTARITY - DETERMINING 2
FRAMEWORK 3.
CONFLEMENTARITY - DETERMINING 3
FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 430; DB
Pred. No. 4.7e
10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MARKHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                8B48A204 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UPDATE)
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. 4.7e-26;
                                                                                                                                                                             DB 1,
5.7e-26;
11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                     Length 108;
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                                                               Query Match
Best Local S
Matches 80
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Best Local S
Matches 81
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SEQUENCE FROM N.A.

MEDLINE; 83131846.

SIEKEVITZ M., GEFTER M.L., BRODEUR P.,

MARSHAK-ROTHSTEIN A.;

EUR. J. IMMUNOL. 12:1023-1032(1982).

-!- FROM ANALYSIS OF THE SIZES OF SEVE

THAT HYBRIDIZE TO THIS ONE, THE AU

THESE V REGIONS HAVE REARRANGED TO

PIR; A02028; HYMSG7.

HSSP; P01789; 6FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
HV03_MO
P01747;
                                                                                                                                                                    CHAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01758;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 81245215.
GIVOL D., ZAKUT R., EFFRON
NATURE 292:426-430(1981).
                                                                                                                                                                                                           IMMUNOGLOBULIN V REGION;
SIGNAL 1 19
CHAIN 20 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN PRECURSOR V REGION (108A).
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE) EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUEN
21-JUL-1986 (REL. 01, LAST ANNOYN
1G HEAVY CHAIN V REGION (36-65).
                                                                                                                                                                                                                                                                                                EMBL; J00488; G554028; PIR; A02041; HVMS8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HV14_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY;
NON_TER 120 120
SEQUENCE 120 AA; 13307 MW; BBA8CCA1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUTHERIA; RODENTIA.
                        113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 VQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
SGKSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLIN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRV---TDWYFDVWGAGTTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN
                                                                                                                                                                                                                                                                               P01789; 1IGI
                                                               90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81;
                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 68.3
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RODENTIA.
                                                                                                                                                               20
117
117
                                                               Conservative
                                                                                                                                                                        ΑΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                        12972
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75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.5%;
68.1%;
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LAST SEQUENCE UI
LAST ANNOTATION
                                                                                SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                K., RECHAVI
                                                             Score 422; DB
Pred. No. 2.1e
8; Mismatches
                                                               8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 424.5;
Pred. No. 1.4e
.4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                      941C002E CRC32;
                                                                                                                                                                                                               HEAVY CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .4e-25;
les 21;
                                                                                                         B
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                                                                                   .1e-25;
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                                                                                                                                                                                                                                                                                                                                                                RAM
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                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                Ö.,
                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 120;
                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAMMALIA;
                                                                                                                                                                                                               (10A)
                                                                                                         117;
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F 21-JUL-1986 (REL. 01, CREATED)

T 21-JUL-1986 (REL. 01, LAST SEQUF

DT 01-OCT-1993 (REL. 27, LAST ANNO

DE IG KAPPA CHAIN V-VI REGION (XRF

OS MUS MUSCULUS (MOUSE).

OS MUS MUSCULUS (MOUSE).
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                                                                                             RAO D.N., RUDIKOFF S., POTTER M.;
BIOCHEMISTRY 17:5555-5559(1978).
-!- THIS CHAIN WAS ISOLATED FROM
                                                                                                                                          MEDLINE; 79082830
RAO D.N., RUDIKOFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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RUDIKOFF S., RAO D.N., GLAUDEMANS C.P.J., POTTER M.;

PROC. NATL. ACAD. SCI. U.S.A. 77.4270-4274 (1980).

-!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UP
01-OCT-1993 (REL. 27, LAST ANNOTATION
1G KAPPA CHAIN V-VI REGION (SAPC 10).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRA
                                                                                                                                                                                     SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                  IMMUNOGLOBULIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
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HEMIS...
THIS CHAIN WALL
R; A01941; KVMSX4.
SEP; P01679; ZFBJ.
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; P01679; 2FBJ.
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Pred. No. 2.6e
11; Mismatches
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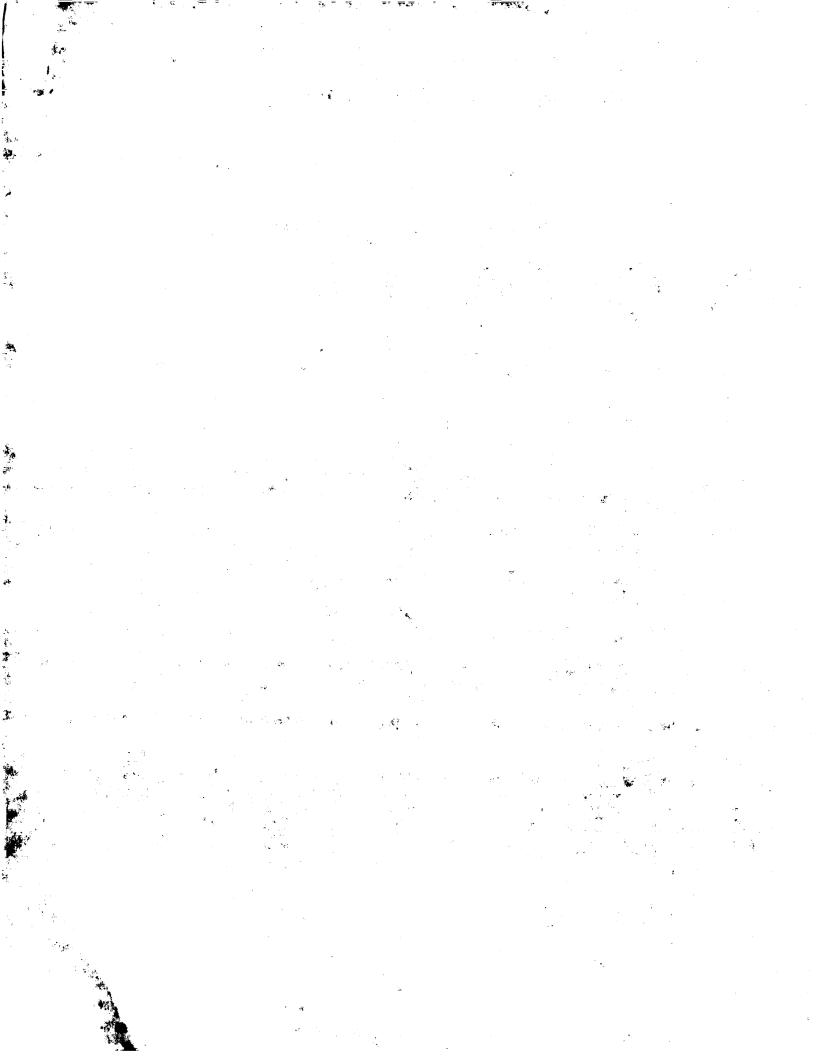
COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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           FRAMEWORK
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                                                                                               MYELOMA
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Matches 78
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21-JUL-1986
01-OCT-1993
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SEQUENCE
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BIOCHEMISTRY 17:5555-5559(1978).
-!- THIS CHAIN WAS ISOLATED FROM
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HSSP; P01679; 2FBJ.
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EUKARYOTA; METAZOA;
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-JUL-1986 (REL. 01, LAST SEQUENCE UP
-CCT-1993 (REL. 27, LAST ANNOTATION
KAPPA CHAIN V-VI REGION (XRPC 24).
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FSGSGSGTSYSLTISSMEAEDAAIYYCQQWNYPLITFGSGTKLEIK
                                                                                                                                      . Similarity 78; Conserv
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73.6%;
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FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3
FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 419; DB Pred. No. 3.1e. 11; Mismatches
                                                                                                                                   Score 414; DB
Pred. No. 7.4e
L1; Mismatches
                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
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Search completed: May Job time: 615 sec

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Result
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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01-NOY-1996 (TREMBLEEL. 08, LAST SEQUENCE UPDATE) 01-NOY-1998 (TREMBLEEL. 08, LAST ANNOTATION UPDATE) V KAPPA (FRAGMENT). V KAPPA (FRAGMENT). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO. [1] SEQUENCE FROM N.A. SUBMITTED (SEP-1990) TO EMBL/GENBANK/DDBJ DATA BANKS. FURT. TOOLSI. (SEP-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.	SULT 2 5535 01-553 01-86	5 LTQSPAILSASDGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYI        :     :      :      :      :      :	Query Match 34.4%; Score 436; DB 10; Length 130; Best Local Similarity 80.0%; Pred. No. 7.4e-25; Matches 84; Conservative 9; Mismatches 10; Indels 2; Gaps 1;	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. JANON K.; SUBMITTED (SEP-1996) TO EMBL/G SUBMITTED (SEP-1996) TO EMBL/G SEQUENCE NO SEGON; SIGNA SEQUENCE 130 AA; 14124 MW;	P80913; 01-NOV-1998 (TREMBLREL. 08, CREATED) 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATI IG KAPPA CHAIN V REGION PRECURSOR. MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.	ALIGNMENTS SULT 1 0913 P80913 PRELIMINARY; PRT; 130 AA.	30 149.5 11.8 50 2 Q15533 Q15533 homo sapien 31 144 11.4 76 2 O75733 O75733 homo sapien 32 143.5 11.3 513 10 P97797 P97797 mus musculu 33 142.5 11.2 503 2 P78324 O75054 homo sapien 34 141.5 11.2 509 10 035924 O76051 homo sapien 35 139 11.0 45 2 O76051 O08907 mus musculu 36 137.5 10.9 509 10 008907 O08907 mus musculu 37 130.5 10.3 509 11 008555 O88555 mus musculu 38 130 10.3 509 10 008555 O88555 mus musculu 39 128.5 10.1 78 2 O75720 O75054 homo sapien 40 128.5 10.1 78 2 O75720 O75054 homo sapien 41 128.5 10.1 78 2 O75720 O75054 homo sapien 42 127.5 10.1 145 2 O16237 O75720 homo sapien 43 127.5 10.1 145 2 O16237 O75736 homo sapien 44 127 10.0 81 2 O75736 O75736 homo sapien 45 122 9.6 258 12 Q90559 O75736 homo sapien

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EMBL; D90161; G1262585; -.

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FISCHER M., KUEPPERS
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SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009535; E1311468; -.
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                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
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O1-NOV-1998 (TREMBLREL. 0
O1-NOV-1998 (TREMBLREL. 0
IG HEAVY CHAIN VARIABLE R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009528; E1311456; -.
NON_TER 1 1 1
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EUKARYOTA; METAZOA; CHORDATA; VEI
PRIMATES; CATARRHINI; HOMINIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 MNWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAV 213
                                                                                                                                                                                                                                                                                                                                                                                                  215 YCARRVIDW---YFDVW 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 NWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVY 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 YYCARRVTDW---YFDVW 228
                                                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                                                                                    FCARHSSSWPIYYFDNW
                                                                                                                                                                                                                                                                                                                                                                                                                                               SWIRQSPGKGLEWIGYIY-YTGSINYNPSLKSRVTISLGTSENQFSLNLTSVTAADTAVY
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78
7 AA;
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                                                  CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.48;
41.08;
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44.2%;
                              HOMINIDAE;
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                                                                                                             08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
REGION (FRAGMENT).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 181; DB 2;
Pred. No. 9.1e-07;
3; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 182.5; DB 2
Pred. No. 7.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intestinal plasma cells
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                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
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Best Local S
Matches 35
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Best Local (
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NON_TER
SEQUENCE
               043234 PRELIMINARY; PRT; Y/ AA. 043234; OTTUN-1998 (TREMBLREL. 06, CREATED) O1-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UP O1-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION RHEUMATOID FACTOR RF-ET13 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             075729
075729;
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human IgA and IgM secreting intestinal plasma cells mutated VH region genes."; SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AJ009520; E1311440; -.
                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                     mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AJ009526; E1311452; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISCHER M.,
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                   FISCHER M., KUEPPERS R.; "Human IgA and IgM secreting
                                                                                                                                                                                                                                                                                                                                                                                         PRIMATES; CATARRHINI; HOMINIDAE; HOMO
                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
             HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                          FISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 WVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYY 215
                                                                                                                                                     212
                                                                                                                                                                                             152
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                                                                                                                                AVYYCVKDGVSANSVWD-YFDYW
                                                                                                                                                     AVYYC----ARRVTDWYFDVW
                                                                                                                                                                        YAMSWVRQAPGKGLEWVSSIDGAGIDTYYAESVKGRFTISRDNSKNTLYLQMNTLRAEDT
                                                                                                                                                                                            HTMNWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDS
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34; Conservative
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78
78 AA;
  METAZOA;
                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KUEPPERS R.;
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              (HUMAN)
                                                                                                                                                                                                                                                                      AA;
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9396
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9075
  CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.1%;
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42.2%;
                                                                                                                                                                                                                                                                      WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                             888
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                                                                                                                                                                                                                                                                                                                                                                                                                                  REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
                                                                                                                                                                                                                  16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                82
                                                                                                                                                                                                                 Score 176.5; DB Pred. No. 2e-06; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                     intestinal plasma
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                                                                                                                                                                                                                                                                      9063B32A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                    VERTEBRATA; MAMMALIA;
  VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
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Mismatches
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                                ON UPDATE)
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                                                                                                                                                                                                                                                                                                                                      cells
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                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA;
                                                                                                                                                                                                                                                                                                                                     carry
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RESULT
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Best Local S
Matches 34
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Best Local S
Matches 31
                   O75724 PRELIMINARY;
O75724;
O1-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
01-NOV-1998 (TREMBLREL. 0
1-NOV-1998 (TREMBLREL. 0
1G HEAVY CHAIN VARIABLE R)
VH.
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MOL. IMMUNOL. 0:0-0(1997).
EMBL; AF035802; G2665882; -
NON_TER 97 97
SEQUENCE 97 AA; 10748 MP
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075726;
01-NOV-1998
                                                                                                                                                                                                                                                                NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                            "Human IgA and IgM secreting intestinal plasma cells mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AJ009523; E1311446; -.
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[1]
 HOMO SAPIENS (HUMAN) EUKARYOTA; METAZOA; (
                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                  OMO
                                                                                                                                                                                                                                                                                                                                                                              PRIMATES;
                                                                                                                                                                                                                                                                                                                                     FISCHER M.,
                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 LQESGPEVVKPGGSMKISCKTSGYSFTGHTM--NWVKQSHCKNLEWIGLINPYNGDTNYN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                    214 YYCARRVTDWYFDVW
                                                                                                                                                                                          154 MWWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAV 213
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                                                                                                                                                                                                                                                                                                                                                                                       SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSLKSRLTISKDTSKSQVVLTMTNMDPMDTATYYCAR
                                                                                                                                 YYCVRDSYDRGFDFW
                                                                                                                                                                        LTWVRQAPGKGLEWVATINEDGGEKYYVDSVKGRFTISRDDATNSLYLQMNSLRAEDTAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                              CATARRHINI;
                                                                                                                                                                                                                                                                  77
                                                                                                                                                                                                                                                                                                                                     KUEPPERS R.;
                                                                                                                                                                                                                Conservative
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9022
  CHORDATA;
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41
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                                      08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE
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                               REGION
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                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 175.5; |
Pred. No. 2.9e
23; Mismatches
                                                                                                                                                                                                              Score 174; DB
Pred. No. 2.9e
L6; Mismatches
                                                                                                                                                                                                                                                                 EB7B458D
                                                                                                                                                                                                                                                                                                                                                                                       VERTEBRATA;
  VERTEBRATA; MAMMALIA;
                                                                                PRT;
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                               (FRAGMENT).
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.9e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97
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                                        UPDATE)
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  EUTHERIA;
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07572998 (TREMBLREL. 08,
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0758401-WOY-1998 (TREMBLREL. 08,
0759401-WOY-1998 (TREMBLREL. 08,
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Best Local S
Matches 29
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075721;
01-NOV-1998 (TRE
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1G HEAVY CHAIN V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human IgA and IgM secreting intestinal mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009521; E1311442; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FISCHER M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FISCHER M., KUEPPERS R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Similarity 50.8%;
32; Conservative 1
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HAIN VARIABLE
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                                                                                                                PRELIMINARY;
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9624 MW;
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. 08, LAST SEQUENCE UPD
. 08, LAST ANNOTATION U
E REGION (FRAGMENT)
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08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EA14CFDF CRC32;
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1 01-NOV-1998 (TREMBLREL RF
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Best Local S
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Best Local S
Matches 31
075727
075727;
01-NOV-1998
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                    VH.
HOMO SAPIENS (HUMAN).
HOMO SAPIENS (HUMAN).
TOBHINI; HOMINIDAE;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "FISCHER M., KUEPPERS R.;
"Human IgA and IgM secreting
mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/
                                                                                                                                                                                                                                                                     TISSUE=INTESTINE;
FISCHER M., KUEPPERS R.;
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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TISSUE-INTESTINE;
                                                                                                                      154 MNWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAV 213
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                                                                                                           MFWVRQAPGKGLEWVALSERDDESTSYADSVKGRFTVSRDISKSTLYLQMSSLRVDDTAV 62
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  (TREMBLREL. 08,
                                                                                                                                                  Conservative
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                     PRELIMINARY;
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. 08, LAST SEQUENCE U. 08, LAST ANNOTATION
.E REGION (FRAGMENT).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
  CREATED)
                                                                                                                                                 Score 168.5; DB
Pred. No. 7e-06;
6; Mismatches
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Pred. No. 6.4e-06;
9; Mismatches 27;
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AE; HOMO.
                     PRT;
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Best Local S
Matches 34
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Best Local Similarity
Matches 35; Conserv
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NON_TER
SEQUENCE
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075741;
01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *FISCHER M., KUEPPERS R.;

"Human IgA and IgM Secriting intestinal plasma cells mutated VH region genes.";

SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009524; E1311448; -

NON_TER 1 1

NON_TER 80 80

SEQUENCE 80 AA; 9351 MW; 63DE158A CRC32;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
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01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009540; E1311476; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-INTESTINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISCHER M., KUEPPERS R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 MNWVKQSHGKNLEWIGLINPYNGDTNYNQKFKGKATFTVDKSSSTAVMELLSLTSEDSAV 213
                                                        214 YYCARRVIDWY-FDVW 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 DSAVYYCAR -- RVTDWYFDVW 228
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                                                                                                                                                                                                                        Local Similarity
nes 34; Conserv
     62
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                                                                                                            MSWVRQAPGKGLEWVSGISGSGDYTYYADSVKGRFTISRDNSKNTLSLQLNSVTAEDTAV 61
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YYCARHYYDSSPFDYW 77
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                                                                                                                                                                                                                                                                                                                                                             8734 MW;
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                                                                                                                                                                                                                  13.1%; Score 165.5; DB 2;
44.7%; Pred. No. 1.2e-05;
tive 13; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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Pred. No. 8.1e-06;
6; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                           1F7F9E8E CRC32;
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Humanised CDR Mus musculus

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Copyright (c) 1993 - 1998 Compugen Ltd
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OM protein protein search, using sw model

May 13, 1999, 09:37:42; Search time 23.53 Seconds (without alignments) 203.715 Million cell updates/sec

Run

Title: Perfect score: Sequence:

US-08-704-178-3
1267
1 MDLQLTQSPAILSASPGEKV.....RRVTDWYFDVWGAGTTVTVS 237

Scoring table: BLOSUM62

Searched: 162890 seqs, 20225328 residues

A\_Geneseq\_34:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

4444 333333333333333333333333333333333	กรอบบ	Result No.
795.5 793.5 784.5 782.5 782.5 782.5 745.5 745.5 736.5 73	<b>7. UIDOI</b> 1	
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R60206 W15186 W15186 W15186 R60443 R7045443 W37085 R804572 W802191 R90549 W70152 W70191 R97380	1020 5182 5442 5784	
Fv(GP-2) immunosup Bispecific CD3-16F Single-chain anti- Sequence of the si Fv(GP-4) immunosup Anti-human SC sing 26-10 sFv. Express Multifunctional pr 18-2-3/TRY202'. Single chain bindi 18-2-3/TRY202'. Sequence of divale CC49/212 SCA PLAP PLAP CC49/212 SCA PLAP PLAP CC49/212 SCA Sequence of a mult single chain bindi TRY104b single chain polyp single chain bindi TRY104b single chain bindi Sequence of the sh single chain bindi TRY104b single chain bindi Chimeric receptor Chimeric receptor Chimeric receptor Chimeric receptor Chimeric receptor Chimeric receptor 14-4-20 VL / 217 / TRY104b. Single po Sequence of single humanised CDR-graf single chain bindi 18-2-3/TRY59 singl Murine 5G1.IM1 scf TRX59 single chain 18-2-3/TRY59. Sin Nematode salivary	ti-erbb ngle-ch ngle-ch quence ti-gpl3	scription

	ALIGNMENTS
R94020	1020
ij	R94020 standard; Protein; 237 AA.
AC	R94020;
DT	21-MAY-1996 (first entry)
DE	Anti-erbB2 scFv.
KW	Oncoprotein; erbB2; cell proliferation; tumour; cancer;
KW	intracellular antibody homologue; single chain antibody; scFv;
KW	
SO	Synthetic
PN	WO9607321-A1.
Дď	14-MAR-1996.
ΡF	23-AUG-1995; U10740.
PR	
PR	
PA	
ΡI	Curiel DT, Deshane J;
DR	WPI; 96-171307/17.
DR	N-PSDB; T17728.
Tq	Inhibition of proliferation or survival of, esp. malignant erbB2,
Id	cells - by introducing nucleic acid mol. encoding antibody homologue
Id	which is expressed and binds, pref. erbB2, protein intracellularly
Sđ	Disclosure; Page 29-30; 48pp; English.
ဂ္ဂ	A nucleic acid comprises a first sequence encoding a signal peptide
င္ပ	(R94019) linked to a second sequence (T17728) encoding a single
ဂ္ဂ	chain Fv fragment (R94020) that binds a human erbB2 oncoprotein.
33	The anti-erbB2 sfv portion is obtained by PCR using e23scfv
გ	plasmid as template. The signal peptide directs the scFv to the
ဂ္ဂ	endoplasmic reticulum. The nucleic acid is incorporated into a
გ	plasmid or viral vector to facilitate expression of the scrv antibody
ဌ	homologue within e.g. an epithelial carcinoma cell. Intracellular
ဂ္ဂ	
ဂ္ဂ	thereby inhibits cell proliferation and cell survival and decreases
G	
•	tumorigenicity.

VQ. RESULT
W15185
ID W1
AC W1
DT 05
DE Si
KW Si
KW bi 밁 δÃ 밁 Q 멁 Query Match 100.0%; Score 1267; DB 1; Best Local Similarity 100.0%; Pred. No. 3.4e-80; Matches 237; Conservative 0; Mismatches 0; W15185 standard; Protein; 237 AA.
W15185;
W15185;
05-JUN-1997 (first entry)
Single-chain anti-erbB2 antibody e23(Fv).
Single chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma; 61 61 RFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEGK 120 RFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEGK 120 0 Gaps

Length 237;

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Best Local S
Matches 237
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07-OCT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
(ARON-) ARONEX PHARM INC.
BITA BY
                          06-JAN-1994.
21-OCT-1992; U08545.
30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY I
Kasprzyk PG, King CR;
WPI; 94-025878/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a claimed single-chain antibody, designated e33(FV), which binds to erbB-2. Monoclonal antibody e23 was generated by immunising mice with N/erbB-2 cells overexpressing the gpl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gpl85 marker, e.g. breast, ovarian and non-small cell lung carcinomas, and, when coupled to a cytotoxic agent, to treat such tumours. Sequence 237 AA;
                                                                                                                                                                                                                                                                              21-JUL-1994 (first entry)
Sequence of the single chain anti-erbB2 antibody, Ab no.23
Single chain anti-erbB1 antibody; cancer therapy; prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bird RE, Kasprzyk PG, WPI; 97-064831/06. N-PSDB; T65006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells expressing this protein Claim 2; Columns 25-28; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single chain antibodies specific for erbB-2 protein, labels or cytotoxin, useful for detection and treatme
                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                       monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                     R45442;
                                                                                                                                                                                                                                                                                                                                                                                               R45442 standard;
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us musculus.
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237; Conser
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llarity 100.0%;
Conservative (
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108. .121
/label= linker
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Pred. No. 3.4e-80;
; Mismatches 0;
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treatment of
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N. PSDB; 791615.

DR N. PSDB; 791615.

DR N. Producing single chain Fv antibody in Escherichia coli - by PT producing single chain Fv antibody, followed by protein folding or by PT expression in an inclusion body, followed by protein folding or by PT co-expression with a chaperonin as a soluble fraction PS Claim 4; Page 6-7; 9pp; Japanese.

CC The sequences given in W25783-84 represent single chain Fv (scFv) CC antibodies which are produced in E. coli. The scFv's are derived CC either by: (1) expression as an inclusion body, followed by folding CC (i.e. by denaturation and solubilisation) or (2) expression as a CC soluble fraction by co-expression with chaperonin. Using the methods, CC scFv can be produced in E. coli, either in a soluble fraction or in CC inclusion bodies. Like the parent double chain antibodies, the scFv polypeptides are useful in immunological diagnosis or for separation CC and purification, but they lessen the side effects caused by antibody constant regions. The availability of scFv polypeptides contributes to fundamental research and development of diagnostic and therapeutic
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Sequence 236 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain Fv; scFv; antibody; E. coli; anti-T3 antibody; anti-gp130 antibody; inclusion body; chaperonin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W25784 standard;
W25784;
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Sequence
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97-474306/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 (first entry) antibody derived scrv.
240
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JP-027622.
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Pred. No. 1.9e-79;
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Best Local Similarity
Matches 166; Conser
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MAb capable of binding to the gamma chain of the IL-2 receptor, and thus of blocking the IL-2 response, is produced by mouse hybridoma line GP-2 (FERM MP-4641). DNA encoding the variable region of this MAb was expressed in E. coli, yielding Fv(GP-2) with immunosuppressive activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fv(GP-2) immunosuppressive. MAb; monoclonal antibody; hybr Fv; antibody variable region;
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Takeshita T
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07-MAR-1994; JP-036065.
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21-APR-1994; 106257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLQLTQSPAILSASPGEKYTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPAR
                                                                                                                                                                                                                                            PARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK-GSTSGSGKSS
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                                                                   TNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYF---DVWGAGTTV
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                                             TNYDEKFKSKATLTVDTSSSTAYMHLSSLTSEDSAVYYCTRSSRNWVYYAMDYWGQGTSV
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ion; GP-2; Fv(GP-2);
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Pred. No. 1.7e
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..7e-52;
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Example 1; Fig 11 and Page 29-31; 50pp; English.

The VL and VH sequences of the anti-CD3 hybridoma G19-4 were amplified by PCR methods. A gene fusion was constructed from the two amplified domains and a (G194Ser)3 linker. The amino terminus of the VL-VH fusion cassette was fused at the SalI site to the L6 light chain variable region leader peptide and the carboxy-terminus was fused directly to the hinge region of the Fc domain at the BcII site and/or to a short "helical" peptide linker to construct the bispecific CD3-L6Fvlg antibody derivative. The variable regions for L6 were fused in frame to the opposite end of the helical linker (not included in R60206).
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Best Local Similarity
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Linsley PS;
WPI; 94-250885/31.
N-PSDB; Q81076.
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10-AUG-1994.
31-JAN-1994;
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13-SEP-1993; US-121054.
(BRIM ) BRISTOL-WIERS SQUIBB CO.
Bajorath J, Fell PH, Gilliland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion protein; recombinant bispecific single chain antibody;
helical peptide linker; anti-L6 antibody; tumour cell antigen;
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Bispecific CD3-L6FvIg
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                                                                                                                                                                                                                                                                                                      VDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGTVKLLIYYTSRLHSGVP
  GAGTTVTVS
                               PYKGLTTYNQKFKGKATLTVDKSSSTAYMELLSLTSEDSAVYYCARSGYYGDSDWYFDVW
                                                                 PYNGDINYNQKFKGKATFTVDKSSSTAYMELLSLISEDSAYYYCARR----VTDWYFDVW
                                                                                                                                                    KG-----VQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLIN
                                                                                                                                                                                                                   SRFSGSGSGTDYSLTIANLQPEDIATYFCQQGNTLPWTFGGGTKLVTKRELGGGGSGGGG
                                                                                                                                                                                                                                          ARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEG
                                                                                                                              SGGGGSIDEVQLQQSGPELVKPGASMTMSCKASGYSFTGYIVNWLKQSHGKNLEWIGLIN
                                                                                                                                                                                                                                                                                                                                                                                            162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
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/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= L6_VL_leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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65.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .302
:l= Fv_helical_linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD3_VL-VH_fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Gly4Ser)3_linker
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                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                       Score 842; DB
Pred. No. 5.8e
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayden
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
.8e-51;
                                                                                                                                                                                                                                                                                                                                                                                            45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 302;
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                                                                                     228
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SC Claim 2; Columns 27-30; 28pp; English.

CThe present sequence represents a claimed single-chain antibody, designated e21(Fv), which binds to erbB-2. Monoclonal antibody e21 was generated by immunising mice with N/erbB-2 cells overexpressing the 9pl85 protein, removing spleen cells and producing hybridomas by standard techniques. Messenger RNA coding for the anti-erbB-2 monoclonal antibody was isolated and converted to cDNA. Regions coding for the heavy- and light- chain variable regions were then amplified by PCR and joined via a sequence encoding a peptide linker. The resulting single-chain antibody is useful for in vitro diagnosis of tumour cells which overexpress the erbB-2 gpl85 and, when coupled to a cytotoxic agent, to treat such tumours.

Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bird RE, Kasprzyk PG, WPI; 97-064831/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-0CT-1991; US-772270.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
(ARON-) ARONEX PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus
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Single chain antibody; variable region; light chain; heavy chain; breast cancer; ovarian cancer; non-small cell lung carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W15186 standard; Protein; W15186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single chain antibodies specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; T65007
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                                                                                                                                                                                                KFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYFDV-----WGAGTTVTV
                                                                                                                                                                                                                                                                                                                                           KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCA---SYYYYSAYYAMYYWGQGTSVTV
                                                                                                                                                                                                                                                          QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155; Conserv
                                                                                                                               237
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anti-erbB2 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
106. .119
/label= linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic agent; erbB-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ific for erbB-2 protein, for detection and treatme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 795.5; DB : Pred. No. 6.9e-48, 2; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR;
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Mus sp.

EP-621338-A.

26-0CT-1994; 106257.

F 21-APR-1994; 106257.

PR 21-APR-1994; JP-094491.

PR 07-MAR-1994; JP-036055.

PR 07-MAR-1994; JP-036055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 155; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R45443 stand
R45443;
21-JUL-1994
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The source of human erbbs-2 protein for the prodn. of antibodies rather source of human erbbs-2 protein on its surface (N. (255180/R45442) is a NIH/3T3 cell engineered to express the human erbb-2 protein on its surface (N. erbb-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbb-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. animals given a combination of the 2 Abs, tumours completely sequence 238 AA;
                                                                                                                                                                                                                     Fv(GP-4) immunosuppressive.
MAb; monoclonal antibody; hybridoma; interleukin-2;
Fv; antibody variable region; GP-4; Fv(GP-4);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-1994.
21-OCT-1992; U08545.
30-JUN-1992; US-906555.
(MOLE-) MOLECULAR ONCOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1994 (first entry)
Sequence of the single chain anti-erbB2 antibody, Ab no.21
Single chain anti-erbB1 antibody; cancer therapy; preventi
                              WPI; 94-325948/41.
N-PSDB; Q73679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of malignancies over 2 monoclonal antibodies which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kasprzyk PG, King
WPI; 94-025878/03.
Immunosuppressant polypeptide
interleukin-2 response
                                                             Takeshita T;
                                                                                                                                                                                                           immunosuppressive.
                                                                                                                                                                                                                                                                           09-MAY-1995
                                                                                                                                                                                                                                                                                                          R60781 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q55181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPARFS
                                                                                                                                                                                                                                                                                                                                                                                                           FKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYFDV------WGAGTTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYNQK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEGKGVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWVYDTSKLASGVPGRFS
                                                                                                                                                                                                                                                                                                                                                                                           FQGKASITADTSSNAAYLQLSSLTSEDTAVYYCA---SYYYYSAYYAMYYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDPK
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                                                                                                                                                                                                                                                                               (first
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                                                                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                               entry)
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                                                                             Nakazawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      over-expressing ERB-[2 - using
hich recognise different epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238
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Pred.
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No. 9.5
             ability
                                                                             Shimamura
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າ.5e-48;
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                                                                             Sugamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at
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PT the serpin enzyme complex receptor, used in gene therapy of the Example 9: Pages 120-121; 158pp; English.

CC This represents an anti-human SC single chain Fv/protamine fusion protein Sequence containing a target binding molety capable of binding molety. CC This can be used in a method for delivering an oligonucleotide to a commandian cell. The method comprises conjugating the target binding cc mammalian cell. The method for delivering an oligonucleotide to a cc mammalian cell. The method comprises conjugating the target binding cc the carrier to an expression vector encoding one or more gene products to form a pharmaceutical composition. A mammalian cell having on its conface SECR, is contacted with the pharmaceutical composition under conditions allowing binding to the interior of the cell. The composition cc and method are used for the introduction of exogenous genetic material cc into target host cells expressing SECR on their surface. The nucleic acid may encode a functional wild-type or mutant gene or may be an antisense sequence or other nucleic acid having a therapeutic properties, cc e.g. enzymatic activity, cytokine activity and antibiotic activity which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Sin
Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9: Page 27-28; 37pp; English.

MAb capable of binding to the gamma chain of the IL-2 recept
thus of blocking the IL-2 response, is produced by mouse byt
line GP-4 (FERM BP-6640). DNA encoding the variable region
this MAb was expressed in E. coli, yielding Fv(GP-4) with
                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                               03-JUN-1996; US-656906.
(UYCA-) UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                                                                                              11-DEC-1997.
03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-human SC single chain Fv/protamine fusion protein. Fusion protein; SC single chain Fv/protamine fusion protein; SECR; exogenous gene; serpin enzyme complex receptor; gene therapy; target binding moiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W37085
                                                                                                                                                                                                                                                                                                  Delivering compacted exogenous nucleic acid to cells
                                                                                                                                                                                                                                                                                                                     N-PSDB; V00611.
                                                                                                                                                                                                                                                                                                                                                    Davis
                                                                                                                                                                                                                                                                                                                                                                                                                             WO9746100-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STQVKLEESGPELVKPGASVKISCKASGYSFTGYYMHWVKQSHVKSLEWIGRINPYNGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLELKVEKSSGSGSESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDILLTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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63.5%;
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Pred.
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Best Local S
Matches 156
                                                                                                                                                                                   (UYCA-) UNIV CALGARY.
Anthony JG, Ng SC, Wo
WPI; 93-152491/18.
N-PSDB; Q41069.
antibody Fv fragments or single chain Fv molecules Disclosure; Fig 6; 51pp; English.
This sequence represents a single chain Fv molecule which contains the heavy and light variable portions (VH and VL) of antidigitoxin monoclonal antibody (MAb) 26-10 (see also R34670-71), a signal sequence (see R38527-28) and a linker between the two variable regions. The DNA sequence encoding this protein was used in the construction of an expression-secretion system for the production of biologically active Fv fragments. The system also contains a DNA sequence encoding the T7 promoter. The secretion-expression vector was produced by polymerase chain reaction Fv fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is delivered to a cell surface via the SECR binding moiety. The nucl acid can be compacted at high concentrations with the carrier molecu a critical salt concentration. The condensation of such complexes provides structural features to the DNA/cationic lipid complex that prolong in vivo expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy; light; variable; VH; VL; region; antidigitoxin; monoclonal; antibody; MAb; 26-10; Fv; fragment; antigen; binding site; linker; expression-secretion system; T7 promoter; signal peptide; molecule polymerase chain reaction; PCR; single chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-10 SFV
                                                                                                                                                       Expression-secretion vectors - for prodn. of biologically active antibody Fv fragments or single chain Fv molecules
                                                                                                                                                                                                                                             16-OCT-1992;
18-OCT-1991;
                                                                                                                                                                                                                                                                          WO9308300-A.
29-APR-1993.
                                                                                                                                                                                                                                                                                                                                                  peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSGGGSEVQLQQSGPDLVKPGASVKISCKTSGYTFIEYTMHWVKQSHGKSLEWIGGINPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVPARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK-GSTSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WGQGTTLTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGAGTTVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGGTSYNQKFKGKATLTVDKSSTTAYMELRGLTSEDSAVYSCAR----YYRYDVLSAMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGDTNYNQKFKGKATFTYDKSSSTAYMELLSLTSEDSAVYYCARRYTDWY-----FDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVPGRFSGSGSGTDFSLNIHPMEEDDTAMYFCQQSKAVPYTFGGGTKLEIKGGGGSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDIVLTQSPASLAVSLGQRATISCRASESVDNYAISFMNWFQQKPGQPPKLLIYAASNQG
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US-777709.
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139. .:
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                                                                                                                                                                                                                                                                                                                                                    .153
                                                                                                                                                                                                                                                                                                                                                                                            "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                "26-10 VL sequence"
                                                                                                                                                                                                                                                                                                       "26-10 VH sequence"
                                                                                                                                                                                                                                                                                                                                     Linker peptide
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No. 6.
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.9e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                  CC The multifunctional protein comprises a single chain biosynthetic Ab CC binding site (comprising sequences minicking the light chain and heavy CC chain variable regions of murine monoclonal 26-10) with the specificity CC of murine monoclonal 26-10, linked through a spacer to the FB fragment of protein A, here fused as a leader, and constituting a binding site for FC CC The spacer contains the 11 C-terminal amino acids of the FB followed by CC Asp-Pro ( a dilute acid cleavage site). The construct contains CC binding sites for both FC and digoxin, and its structure can be used for specific binding assays, affinity purificn. biocatalysts, targetting, CC imaging an immunological treatment of oncogenic and infectious diseases. CC imaging an immunological treatment of oncogenic and infectious diseases. CC improved stability. It reaches target tissues rapidly and its quickly cleared from the body. It also has reduced immunogenicity and its design CC facilitates binding to other moieties in drug targetting and imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Mat
Best Loca
Matches
Query Match
Best Local Similarity 58.5
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Recombinant multifunctional protein - having antibody binding sequence for biological activity, ion sequestering or binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1988.
19-MAY-1988; U01737.
21-MAY-1987; US-052800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multifunctional protein.
Multifunctional protein; biosynthetic
murine monoclonal 26-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising only the VH or VL regions, and single chain molecules be used to specifically bind one or more of the same antigens as full length antibody from which they are derived.

Sequence 272 AA;
                                                                                          applications.
Sequence 251
                                                                                                                                                                                                                                                                                                                                                        Disclosure; 15pp;
                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; N80178
                                                                                                                                                                                                                                                                                                                                                                                                                               (CREA-) Creative Biomolecules Huston JS, Oppermann H; WPI; 88-353928/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multifunctional Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P80152 standard; protein; 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 DLQLTQSPAILSASPGEKVTMTCRATPSV-----SYMHWYQQKPGSSPKPWIYTTSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGVPARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK--GSTS-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYNGDTNYNQKFKGKATFTYDKSSSTAYMELLSLTSEDSAYYYCA-RRYTDWYFDVWGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLNWYLQKAGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYSGVTGYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSGNKWAMDYWGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIKRGGSGSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                         English
                            58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.0%;
60.2%;
              ; Score 746; DI
; Pred. No. 1.86
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
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Pred. No. 1.4e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody binding site;
                            DB 1;
.8e-44;
                 57;
                                          Length 251
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               Indels
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               12;
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to a
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               Gaps
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RESULT
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                                                                                                                 Query Match
Best Local S
Matches 144
                                                                                                                                                                                       for labelled or immobilised antibody, are less immunogenic, easier to engineer, more stable and less expensive Example 9; Fig 39A-B; 78pp; English.

Computer-designed construct 18-2-3/TRY202' (W02191), encoded by the DNA sequence given in T36463, comprises the variable regions of the light and heavy chains of anti-fluorescein monoclonal cantibody (Mab) 18-2-3 linked by a peptide designed to fit into a groove on the backside of the variable domain structure. The DNA construct was inserted into vector pGX3703 and introduced into E. coli. 18-2-3/TRY202' was produced as a single chain molecule. It cexhibited biological binding activity equivalent in specifically and affinity to that of the original MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY 1996.
02-SEP-1986; US-902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAR-1999; US-299617.
25-APR-1990; US-299617.
25-APR-1990; US-040440.
                                                                                                                                                                                                                                                                                                                                                                                                Bird RE, Hardman K,
WPI; 96-259060/26.
N-PSDB; T36463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-1996 (first entry)
18-2-3/TRY202' single chain binding protein.
18-2-3/TRY202' monoclonal antibody; MAD;
single chain antibody; immunoassay; fluorescein; 18-2-3/TRY202';
single chain binding protein.
Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995; US-468988
(ENZO-) ENZON LABS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric synthetic
                                                                                                                                                                                                                                                                                                                                                                                 Immunoassay using single chain antigen binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111
   61
                            59
                                                                                                                 Local Similarity 59.8 les 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                        MDLQLTQSPAILSASPGEKVTMTCRATPSV--SYMHWYQQKPGSSPKPWIYTTSNLASGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INPYNGDTNYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCA-RRVTDWYFDVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGSGKSSEGKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLNWYLQRAGQSPKLLIYKVSNRF
PARFSGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG-
               PARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTTVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIKRGSGGGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVPARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIK-----GST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLQLTQSPAILSASPGEKVTMTCRATPSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
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58
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                                                                                                                                  239
                                                                                                                   40;
                                                                                                                Score 745; DB 1;
Pred. No. 2e-44;
40; Mismatches !
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                                                                                                                   50;
                                                                                                                                               Length 239;
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7 O2 SEP-1986; US-902971.
7 O2 SEP-1986; US-902971.
7 O2 SEP-1987; US-90210.
7 O2 SEP-1987; US-90210.
7 O2 SEP-1989; US-929617.
7 O2 SEP-1989; US-299617.
7 O2 SEP-1989; US-299617.
7 O2 SEP-1989; US-299617.
7 O2 SEP-1989; US-929617.
7 O3 SEP-1989; US-929617.
7 O3 SEP-1986; US-929617.
7 O3 SEP-1986; US-929617.
7 O3 SEP-1986; US-929617.
7 O3 SEP-1986; US-92971.
7 O4 SEP-1986; US-929617.
7 O4 SEP-1986; US-929617.
7 O4 SEP-1986; US-929617.
7 O5 SEP-1986; US-929711.
7 O5 SEP-198712.
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Sim
Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for a given antigen (Fluorescein). It comprises a first polypeptide comprising the antigen binding portion of of the light chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the heavy chain variable region of an antibody and at least one peptide linker linking the first and second polypeptide chains. The resulting single chain polypeptide can be used in diagnostics, therapy (in vivo and in vitro), imaging, purifications and biosensors. This particular single chain binding molecule was designated 18-2-3Jrmx202' and contains one linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-1994 (first entry)
Single chain polypeptide with affinity for fluorescein.
Monoclonal antibody: MAb; affinity; binding; antigen; d
therapy; imaging; purification; biosensors.
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US5260203-A.
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                                                                                                                                PARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDT
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                                             NYNSALMSRISISKONSKSQVFLKMNSLQIDDTAIYYCAKRIGRIFYYAMDYWGQGTSVT
                                                                                        NYNOKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYF----DVWGAGTTVT
                                                                                                                                                                                                                           PARFSGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG--SE
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                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 742; DB
Pred. No. 3.2e
39; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
.2e-44;
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RESULT
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Example 9; Fig 39; 78pp; English.

A DNA construct (713739) codes for single chain binding molecule

18-2-yTRY2020' (R99649), in which VL and VH regions of anti-

19 Index composed primarily of alternating Gly and Ser residues, with

C Glu and Lys residues to enhance solubility. The construct was

c expressed in E.coli. Soluble, folded chain antibody (SCA) was

c obtd. which was capable of exhibiting a biological binding activity

equivalent in specificity and affinity to that of a monoclonal

c antibody. SCAs (see also R99645-48 and T99650-51) have the

advantages of smaller size, greater stability and reduced cost.
                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUL-1996.
02-SEP-1986; 902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-299617.
25-APR-1990; US-512910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain binding molecule 18-2-3/TRY202'.
Antibody engineering; single polypeptide chain binding single chain antibody; SCA; heavy chain; light chain; monoclonal antibody; MAb; immunoaffinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immuno:purificn. using single binding chain antigen-binding parts of antibody light and regions connected by a linker - is smaller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bird RE, Hardman K, WPI; 96-333309/33. N-PSDB; T13739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R99649
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06-JUN-1995; US-468992
(ENZO-) ENZON LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5534621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric synthetic
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                                                                                                                                                                                                                                                                        Local Similarity
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٧S
                        VS
                                                                                                  SKSTQLKESGPVLVAPSQSLSITCTVSGFSLTNYGVHWVRQPPGKGLEWLGVIWA-GGNT
                                                                                                                GKGVQLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDT
                                                                                                                                                      PARFSGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG--SE
                                                                                                                                                                     PARFSGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSE
                                                  NYNSALMSRLSISKDNSKSQVFLKMNSLQIDDTAIYYCAKRLGRIFYYAMDYWGQGTSVT
                                                              NYNQKFKGKATFTVDKSSSTAYMELLSLTSEDSAVYYCARRVTDWYF---DVWGAGTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /TRY202'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
239
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                        58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ladner
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                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                           Score 742; DB
Pred. No. 3.2e
39; Mismatches
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Search completed: May 13, 1999, 10:02:41 Job time: 1499 sec

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RESULT 1

PC4402

Apten-specific single-chain antibody variable fragment and alkaline phosphatase:

C:Species: Escherichia coli

C:Date: 03-Sep-1998 #sequence\_revision 03-Sep-1998 #text\_change 03-Sep-1998

C:Accession: PC4402

R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.

J. Biochem. 122, 322-339, 1997

A;Title: Construction, bacterial expression, and characterization of hapten-specify A; Reference number: PC4402

A;Accession: PC4402

A;Atatus: preliminary

A;Residues: 1-287 <SUZ>

fusi

bacterial expression, and characterization of hapten-specific

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A;Cross-references: EMBL:x82690; NID:g673439; C;Genetics:
A;Introns: 16/1
A;Superfamily: immunoglobulin V region; immunoC;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                 RESULT 2

$52445

$5245

Ig heavy chain V region precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-May-1995 #sequence_revision 21-Jul-1995
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                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <BER>
                                                                                                                                                                         A; Reference number: S52445
A; Accession: S52445
                                                                                                                                                                                                     C;Accession: $52445
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase
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Query Match
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                                             immunoglobulin V region; immunoglobulin homology
terotetramer; immunoglobulin
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Score 526;
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Ig kappa chain V region - mouse
C; Species: Mus musculus (house mouse)
C; Date: 15-Feb-1991 #sequence_revision 13-Sep-1991 #text_change 20-Mar-1998
C; Accession: A34871
R; Chaudhary, V.K.; Batra, J.K.; Gallo, M.G.; Willingham, M.C.; FitzGerald, D.J.; Past: Proc. Natl. Acad. Sci. U.S.A. 87, 1066-1070, 1990
A; Title: A rapid method of cloning functional variable-region antibody genes in Esche: A; Reference number: A34871; MUID: 90138938
A; Reference number: A34871; MUID: 90138938
A; Accession: A34871
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-120 <CHA>
A; Cross-references: GB:M34000
A; Note: the authors translated the codon TTT for residue 88 as Pro
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                         Ig light chain V region ($107/VH11 group 2-36) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: P70398
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated $107 VH11-encoded anti-DNA autoantibodi
A;Reference number: P70376
A;Accession: P70398
A;Accession: P70398
A;Molecule type: DNA
A;Residues: 1-107 <BEH>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin
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les 104; Conservative
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                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGKSSEGKGVQLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGTSVTVSS 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGTLVTVSA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGVNSE----VQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYWVKQRPEQGLEWIGWID
                                                                                   Conservative
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86.1%;
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                                                                                 Score 496; DB 2; 1
Pred. No. 2.1e-31;
5; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 520.5; DB 2;
Pred. No. 3.3e-33;
8; Mismatches 7;
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5; Mismatches 14;
                                                                                                                   Length 107;
                                                                                 Indels
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C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Sep-1997
C;Accession: S25058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop : A;Reference number: S25057
A;Accession: S25058
A;Status: preliminary
A;Status: preliminary
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A;Residues: 1-235 <FIS>
A;Cross-references: EMBL:X67211; NID:g54828; PID:g54829
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                                                                                                                                     QQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDPKF 182
                                                                                                                                                                         SGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRADAAPTVSI-----F
                                                                                                                                                                                                 SGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGVQL 122
                                                                                                                                                                                                                                                       LTQSPAIMSASPGEKVTMTCSASSSVSKMQWYQQKSGTSPKRWIYDTSKLASGVPGRFSG
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                                                           QGKASITADTSSNAAYLQLSSLT-SEDTAVYYCASYYYYSAYYAMYYWGQGTSVTVSSY
                                                                                                   PPSSEQLTSGGASV--VCFLNNFYPKDINVKWKIDGSER
                         ---NSWTDQDSKDSTYSMSSTLTLTKD-----EYERHNSYTCEATHKTSTSPIVKSF
                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                     Score 491.5; DB 2; Pred. No. 1.1e-30;
                                                                                                                                                                                                                                                                                                                                   Mismatches
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Length 235;

Indels

35;

Gaps

6,

85 62

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A;Title: Characterization of somatically mutated S107 VH11-encover, R;Reference number: PT0376
A;Accession: PT0402
A;Molecule type: DNA
A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig light chain V region (S107/VH11 group 2-17) - mouse (fragment) c;Speciles: Mus musculus (house mouse) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993 C;Accession: PT0402
4 LTQSPAIMSASXGEKVTMTCSASSSVSYMHWYQQKSSTSPKLWIYDTSKLASGVPGHFSG
                            3 LTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWVYDTSKLASGVPGRFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                     somatically mutated S107 VH11-encoded anti-DNA autoantib
                                                                                                                              Score 492; DB 2;
Pred. No. 4.3e-31;
                                                                                                                                                          Length 107;
                                                                                                       Indels
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                                                                                                    Gaps
63
                                                     62
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A;Cross-references: EMBL:X14624; NID:g52029; PID:g52030 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG> F;20-136/Product: Ig heavy chain V region (fragment) #status predicted
Ig light chain V region (S107/VH11 group 2-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                           RESULT
PT0400
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A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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A; Residues: 1-136 < KOF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: PT0403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g light chain V region (S107/VH11 group 2-19) - mouse (fragment)
;Species: Mus musculus (house mouse)
;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
;Species: Mus musculus (house mouse)
;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Feb-1998
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Best Local Similarity
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                                                                                                                                      SGSGNSYSLTISSMEAEDAATYYCYQGSGYPTTFGSGTKLEIK 105
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                                                                                                                                                                                                                    LTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSSTSPKLWICDTSKLASGVPGRFSG 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PT0403
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Pred. No. 1.2e-30;
6; Mismatches 17
                                                                                                                                                                                                                                                                                                                   Score 486; DB 2;
Pred. No. 1.2e-30;
                                                                                                                                                                                                                                                                                                     Mismatches
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30-Sep-1993 #text_change 30-Sep-1993
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A; Molecule type: DNA
A; Residues: 1-107 <BEH>
A; Residues: 1-107 <BEH>
C; Superfamily: immunoglobulin V region;
C; Keywords: immunoglobulin
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R:Behar, S.M.; Lustgarten, D.L.; Corbet,
J. Exp. Med. 173, 731-741, 1991
                                                                                                                                R;Jarrin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G
FEBS Lett. 354, 169-172, 1994
A;Title: A synthetic peptide with anti-platelet activity derived
A;Reference number: S51210
A;Accession: S51210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;MoLecule type: DNA
A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V
C;Keywords: immunoglobulin
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Ig light chain V region (S107/VH11 group 2-2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep_1993 *sequence_revision 30-Sep-1993 *text_change 30-Sep-1993
                                                                                                                                                                                                                               Ig kappa chain V region (AC7) - mouse C;Species: Mus musculus (house mouse) C;Date: 01-Aug-1995 #sequence_revision C;Accession: S51210; S58928
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A; Accession: PT0400
                                      A; Molecule type: protein A; Residues: 1-20 < JAR2>
                                                                                              A; Molecule type: mRNA
A; Residues: 9-99 < JAR>
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                                                                            A; Accession: S58928
Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
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Pred. No. 2.5e-30;
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Pred. No. 2.5e-30;
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Ig light chain V region (S107/VH11 group 2-10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-
C;Accession: PT0397
R;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
J. Exp. Med. 173, 731-741, 1991
A;Title: Characterization of somatically mutated S107 VH11-encoded A;Reference number: PT0376
A;Accession: PT0377
A;Molecule type: DNA
A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                               A; Accession: S07453
A; Molecule type: protein
A; Residues: 1-43 < ROC2>
C; Superfamily: immunoglobu
C; Keywords: heterotetramer
                                                                                                                                                                                                            A; Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of fo hypervariable regions.
A; Reference number: S03471; MUID:84057768
A; Reference number: S03471
A; Rocession: S03471
A; Roclecule type: mRNA
A; Residues: 7-120 <ROCl>
A; Roclecule type: mRNA
A; Roclecule type: m
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EMBO J. 2, 867-872,
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Best Local S
Matches 89
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;Species: Mus musculus (house mouse)
;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
;Accession: PT0397
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Best Local Similarity
Matches 90; Conserv
                                                                            Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
Query Match
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l Similarity 86.4%;
89; Conservative
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pred. No. 3.5e-30;
pred. No. 3.5e-30;
  Score 475;
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Best Local
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                                                                                  66
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                            QGTSVTVSS
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C; Accession: S29594
R; Seymour, R.
submitted to the EMBL Data L
A; Reference number: S29593
A; Accession: S29594
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
PT0395
Ig light chain V region (S107/VH11 group 2-16) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 3
C;Accession: PT0395
C;Accession: PT0395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-107 <BEH>
C;Superfamily: immunoglobulin V region; immunoglobulin
                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:x57857; C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: immunoglobulin C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Characterization of A;Reference number: PT0376 A;Accession: PT0395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Behar, S.M.; Lustgarten, D.L.; Corbet, J. Exp. Med. 173, 731-741, 1991
                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-178 <SEY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 37.3
Best Local Similarity 85.4
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                   111 SGKSSEGKGVQLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 PKFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYMGQGTSYTVSS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 SGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LIQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSSTSPKVWIYDTSKLASGVPGRFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWVYDTSKLASGVPGRFSG 62
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                                           PANGYTEYDPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTGGNY---AYGMDYWG
                                                               PENGNTVYDPKFQGKASITADISSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWG 230
                                                                                                                            TGVNSE----VQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSGNSYALTISNMEAEDVATYYCFXGXGFPLTFGGGTTLELK 106
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96; Conserv
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85.4%;
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                                                                                                                                                                                                                                                                                                                                              NID:g52590;
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                                                                                                                                                                                                    Score 470; DB 2; Lengum and Pred. No. 3.5e-29; Indels
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Pred. No. 1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 9.6e-30;
4; Mismatches 18;
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Search completed: May 13, 1999, 10:03:48 Job time: 1380 sec

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KV1L\_HUMAN KV5N\_MOUSE

P01604 homo sapien P01647 mus musculu

OM protein protein search, using sw model

Run мау 13, 1999, 10:05:48 ; Search time 16.53 Seconds (without alignments) 389.696 Million cell updates/sec

US-08-704-178-4 1271

Title: Perfect score:

Sequence: 1 MQLTQSPAIMSASPGEKVTM.....SAYYAMYYWGQGTSVTVSSY 240

Scoring table: BLOSUM62

Searched: 74019 segs, 26840295 residues

Database : SwissProt\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result

ρy 뭥 Qy

Query Match Best Local S Matches 86

y Match 35.4%; Local Similarity 83.5%; nes 86; Conservative

Score 450; DB 1; I Pred. No. 2.1e-28; 6; Mismatches 11;

Length 107; Indels

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Gaps

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64

SGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIK 105

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SQ	FT	FT	Ή	ΗŢ	FΤ	ΕT	H	FΤ	KW	DR.	DR	င္ပ	먑	RΑ	RX	RP	RN	გ	გ	SO	DE	Ŋ	ΔĬ	ΤŢ	a	Ĭ	KV6F	RESULT		
SEQUENCE	DISULFID	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	DOMAIN	IMMUNOGLOBULIN V	HSSP; P01679;	EMBL; K0073	-!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.	NATURE 304:320-324(1983).	KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;	MEDLINE; 83	SEQUENCE FF	Ξ	EUTHERIA; RODENTIA.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	MUS MUSCULUS (MOUSE)	IG KAPPA CHAIN V-VI	01-OCT-1993	13-AUG-1987	13-AUG-1987	P04940;	KV6F_MOUSE	KV6F_MOUSE	1		
107 107 AA;	23	97	88	56	49	34	24	۳		'9; 1FVB.	K00735; G196435;	N: ANTI-	320-324(	1., GRIFF	83271467.	FROM N.A.		CODENTIA.	METAZOA;	IS (MOUSE	IAIN V-VI	(REL.	(REL.	(REL.		STAN				
107 11561 M	87	106	96	87	55	48	33	23	REGION; HY		35;	2-PHENYL	1983).	ITHS G.M					CHORDAT	·	REGION	LAST		05, CREATED)		STANDARD;				
MW; 1BCOC	BY SIMILARITY	FRAMEWORK	COMPLEM	FRAMEWORK 3.	COMPLEM	FRAMEWORK 2.	COMPLEM	FRAMEWORK 1.	HYBRIDOMA.			OXAZOLON		., MARKHA					A; VERTEB		(NO2-17.4.1).	ANNOTATION UPDATE)	LAST SEQUENCE UPDATE)	ED)		PRT;			ALIGNMENTS	
1BC0C1E3 CRC32;	LARITY.	RK 4.	ENTARITY	RK 3.	ENTARITY	RK 2.	ENTARITY	RK 1.				E (PHOX)		M A.F.,					RATA; TE		.1).	N UPDATE	UPDATE)			107 AA.			MENTS	
2;	٠		COMPLEMENTARITY-DETERMINING		COMPLEMENTARITY-DETERMINING		COMPLEMENTARITY-DETERMINING					ANTIBODY		MILSTEIN					TRAPODA;			<u> </u>								
			VING 3.		NING 2.		NING 1.							C.;					MAMMALIA											
																			ς.											

RESULT 2

KV6J\_MOUSE STANDARD; PRT; 107 AA.

ID KV6J\_MOUSE STANDARD; PRT; 107 AA.

AC P04944;

DT 13-AUG-1987 (REL. 05, CREATED)

DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)

DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)

DE 1G KAPPA CHAIN V-VI REGION (NQ5-78.2.6).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;

OC EUTHERIA; RODENTIA. TWR RAY OCCUPANT OCCU SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

X MEDLINE; 83271467.

X MEDLINE; 83271467.

A KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;

LL LUNGTON: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

C -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.

EMBL, K00744; G196453; -.

DR HSSP; P01679; 1FVB.

DR HSSP; P01679; 1FVB.

KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.

KW IMMUNOGLOBULIN V REGION; FRAMEWORK 1.

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RESULT 4
KV6G_MOUSE
IQ KV6G_MOUSE
AC P04941;
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Best Local
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MEDLINE; 83271467

KAARTINEN M., GRIFFITHS G.M., MARKHAM A.

NATURE 304:320-324(1983).

-!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (P
EMBL; K000740; G196445;

HSSP; P01679; 1FVB.

IMMUNOGLOBULIN V REGION; HYBRIDOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P04943;
13-AUG-1987
13-AUG-1987
01-OCT-1993
IG KAPPA CHAMUS MUSCULUS
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NON_TER
SEQUENCE
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-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
-COT-1993 (REL. 27, LAST ANNOTATION UPDATE)
KAPPA CHAIN V-VI REGION (NQ6-8.3.1).
S MUSCULUS (MOUSE).
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SGSATSYSLTITSMQAEDAATYYCQQWSSNPLTFGSGTKLEXK
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                                                                                                                                             SGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIK 105
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5; Mismatches
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Pred. No. 5.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
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COMPLEMENTARITY-DETERMINING
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Pred. No. 4.3e-28;
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
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                       PRT;
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RESULT 5
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Best Local (
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P04942;
13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-VI REGION (NQ5-61.1.2).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAL
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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SEQUENCE FROM N.A.

REDLINE; 83271467.

KAARTINEN M., GRIFFITHS G.M.,

NATURE 304:320-324(1983).

-!- FUNCTION: ANTI-2-PHENYL OJ

EMBL; K00737; G196439; -.

HSSP; P01679; 1FVB.

IMMUNOGLOBULIN V REGION; HYBR.
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DOMAIN
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 83271467.
KAARTINEN M., GRIFFITHS
NATURE 304:320-324(1983)
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DOMAIN
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13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-VI REGION (NQ2-48.2.2).
MUS MUSCULUS (MOUSE).
EUKREYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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   11605
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82.5%;
                                                                                                                                                                                                                                                                                    G.M.,
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                                                                                                                                                                                           HYBRIDOMA
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 WW;
                                                   COMPLEMENTARITY-DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3
FRAMEWORK 4.
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                                                                                                                                                                                                                                                 OXAZOLONE
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COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
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COMPLEMENTARITY-DETERMINING
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 1CF3CE8D CRC32;
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No. 6.1e-28;
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AC P0167
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Best Local S
Matches 84
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Best Local :
                                                                                                             IG KAPPA CHAIN V-VI R
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                       P04945;
13-AUG-1987 (REL. 0
13-AUG-1987 (REL. 0
01-OCT-1993 (REL. 2
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21-JUL-1986
01-OCT-1993
IG KAPPA CHA
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BIOCHEMISTRY 17:5555-5559(1978).
-!- THIS CHAIN WAS ISOLATED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
MEDLINE; 79082830
RAO D.N., RUDIKOFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE) EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P01676;
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  SEQUENCE FROM N.A. MEDLINE; 83271467. KAARTINEN M., GRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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-JUL-1986 (REL. 01, LAST SEQUEN
-OCT-1993 (REL. 27, LAST ANNOTA
KAPPA CHAIN V-VI REGION (XRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
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  GRIFFITHS
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05, LAST SEQUENCE UPDATE)
27, LAST ANNOTATION UPDAT
VI REGION (NQ2-6.1).
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                                                                                                                                       CHORDATA;
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  G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
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ANNOTATION UPDATE)
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FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3
FRAMEWORK 4.
BY SIMILARITY.
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Pred. No. 1.7e-25;
6; Mismatches 12;
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Pred. No. 6.1e-28;
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  MARKHAM
                                                                                                                                       VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                       PRT;
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  A.F.,
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                                                                                                                                       TETRAPODA; MAMMALIA;
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  MILSTEIN
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  c.;
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RESULT 8
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Best Local :
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Best Local
                                                                            Matches
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DOMAIN 24 33 COMPLEME
DOMAIN 34 48 FRAMEWOR
DOMAIN 34 48 FRAMEWOR
DOMAIN 49 55 COMPLEME
DOMAIN 56 87 FRAMEWOR
DOMAIN 88 98 COMPLEME
DOMAIN 88 98 COMPLEME
DOMAIN 99 108 FRAMEWOR
DISULFID 23 87 BY SIMII
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21-JUL-1986
01-OCT-1993
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DISULFID
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SEQUENCE
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EMBL; K00746; G554059; -.
HSSP; P01679; 1BAF.
                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                 RAO D.N., RUDIKOFF S., POTTER M.;
BIOCHEMISTRY 17:5555-5559(1978).
-1- THIS CHAIN WAS ISOLATED FROM
PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                 KV6A_MOUSE P01675;
                                                                                                                                                                                                                                                                         MEDLINE; 79082830 RAO D.N., RUDIKOFI
                                                                                                                                                                                                                                                                                                                EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                        MUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA;
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                                                                                                                                                                                                                                                                                            SEQUENCE
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-JUL-1986 (REL. 01, LAST SEQUENCE UF-
-JUL-1993 (REL. 27, LAST ANNOTATION
KAPPA CHAIN V-VI REGION (XRPC 44).
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                                    SGSGNSYSLTISSMEAEDAATYYCYQGSGYP-FTEGSGTKLEIK 105
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77.1%;
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                                                                          Score 409; DB 1;
Pred. No. 2.9e-25;
7; Mismatches 12
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Pred. No. 2.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING
                                                                                                                                                      COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                                                                FRAMEWORK 1
                                                                                                                                                                                                                                                                                                                        VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                           2E7F7479 CRC32;
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                                                                                                                                             SIMILARITY.
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Best Local
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P01677;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHALN V-VI REGION (TEPC 601 AND TEPC
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                              MEDLINE; ERUDIKOFF SPROC. NATI
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DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                        SEQUENCE (TEPC 601).
MEDLINE; 79082830.
RAO D.N., RUDIKOFF S., POTTER M.
BIOCHEMISTRY 17:5555-5559(1978).
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DOMAIN
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RUDIKOFF S., RAO D.N., GLAUD PROC. NATL. ACAD. SCI. U.S.A -! THIS CHAIN WAS ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN V-VI REGION (SAPC 10).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                  SEQUENCE (TEPC 191).
MEDLINE; 81054757.
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HSSP; P01679; 2FBJ.
IMMUNOGLOBULIN V REG:
                                                                                                               RUDIKOFF S., RAO D.N.,
PROC. NATL. ACAD. SCI.
-!- THE TWO SEQUENCES A
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HSSP; P01679; 2FBJ.
MMWOOGLOBULIN V REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA;
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                                                                                         GALACTAN.
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                              A01941; KVMSX4.
; P01679; 2FBJ.
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U.S.A. 77:4270-4274(1980).
LATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN
                                                                                                                                                                          GLAUDEMANS C.P.J., POTTER U.S.A. 77:4270-4274(1980).
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COMPLEMENTARITY-DETERMINING 1
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2
FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3
FRAMEWORK 4.
BY SIMILARITY.
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                                                                                                                  FROM MYELOMA PROTEINS
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601 AND TEPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191).
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RESULT 12
HY02_MOUSE STANDARD; PRT; 140 AA
ID HY02_MOUSE STANDARD; PRT; 140 AA
AC P01746;
DT 21-JUI-1986 (REL. 01, CREATED)
DT 21-JUI-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-996 (REL. 34, LAST ANNOTATION UPDATE)
E IG HEAVY CHAIN PRECURSOR V REGION (93G7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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Matches
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Best L
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21-JUL-1986 (REL. 01, LAS
21-JUL-1986 (REL. 01, LAS
1G HEAVY CHAIN V REGION (
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORD
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 83131846.
CTEXEVITZ M., GEFTER M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HV03_MOUSE
P01747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                      SIEKEVITZ M., GEFTER M.L., BRODEUR P., RIBLET R.,
MARSHAK-ROTHSTEIN A.,
EUR. J. IMMUNOL. 12:103-1032(1982).
I. IMMUNOL. 12:103-1032(1982).
I. FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED
THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL C
THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.
                                                                                                                                                                                                                                                                       PIR; A02028; HVMSG7.
HSSP; P01789; 6FAB.
                                                                                                                                                                                                                                                           IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match
| Local Similarity
| Ches 82; Conserv
                                                                                                                180 PKFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYYSAYYAMYYWGQGTSVTVSS
                                                                                                                                                        120 VQLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYD
                                                                                                                                                                                              y Match
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                                                                                                      EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYYFDYWGQGTTLTVSS
                                                                                                                                             VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSGNSYSLTISSMEAEDAATYYCYQGSGYP-FTFGSGTKLEIK
                                                                                                                                                                                      76;
                                                                                                                                                                                                 Similarity
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120 #
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13307
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107
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                                                                                                                                                                                              31.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                     16;
                                                                                                                                                                                     Score 406; DB
Pred. No. 5.7e
l6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8,
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Pred. No. 4.2e-1
8; Mismatches
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
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COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                                              DB 1;
.7e-25;
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                                                                                                                                                                                      28;
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RESULT
KV6E_M
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Best Local Similarity
Matches 78; Conser
                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE; 88317852.
SUH S.W., BHAT T.N., NAVIA M.A., COHEN G
DAVIES D.R.;
PROTEINS 1.74-80 (1986).
-!- THIS CHAIN WAS ISOLATED FROM A MYELO;
PIR; A01942; KWASJ5.
PDB; 2FBJ; 15-OCT-90.
DOMAIN
DISULFID
NON_TER
STRAND
                                                                     DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 21, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-VI REGION (J539).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METRAZOA; CHORDATA; VERTEBRATA; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE: 81054757.
RUDIKOFF S., RAO D.N.,
PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 82152818.
SIMS J., RABBITTS T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A02028; HVMSG7.
HSSP; P01789; 6FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCIENCE 216:309-311(1982).
EMBL; J00493; G195007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=A/J;
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                                                                                                                                                                  DOMAIN
                                                                                                                                                                                    IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KV6E_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132
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20
140
140 AA;
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24
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   REGION;
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15514 MW;
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140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.6%;
                                                                                                                                                                                                                                                                                                                                                                        GLAUDEMANS C.P.J., POTTER M.;
U.S.A. 77:4270-4274(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESTESS
                                                                                                                                                                                  3D-STRUCTURE
                                                                                                                                                                                                                                        FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 401.5; DB 1
Pred. No. 1.5e-24;
                                                                                                                             COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                      COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                         COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
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                                                                                                                                                                  FRAMEWORK
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                                                                                                                                                                                                                                                                                                  RAO
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                                                                                                                                                                                                                                                                                                D.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUCKER P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                          BIND GALACTAN
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                                                                                                          N
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RESULT
HV07_MC
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Best Local S
Matches 79
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MOUSE
HV07_MOUSE
STANDARD;
PRT; 139 AA.
P01751; p01752;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT 1996 (REL. 34, LAST ANNOTATION UPDATE)
01-OCT 1996 (REL. 34, REGION (B1-8 / 186-2).
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TURN
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DOMAIN
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SEQUENCE
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TURN
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CHAIN
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                                                                                                                                                                                                                                                                                                      BALTIMORE D.;
CELL 24:625-637(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                          PIR; A0
                                                                                                                                                                                                                                         EMBL; J00529;
                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; RODENTIA.
                                                                                                                                               DOMAIN
                                                                                                                                                                                              IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                         ·1- THE B1-8
                                                                                                                                                                                                                                                                                                                                      BOTHWELL A.L.M., PASKIND
                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 81234548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWYYDTSKLASGVPGRFSG
                                                                                                                                                                                                                                                           ANTIBODIES!
                                                                                                                                                                                                                                                                        THE B1-8 MU CHAIN ANTIBODIES TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSGNSYSLTISSMEAEDAATYYCYQGSGYP-FTFGSGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTQSPAITAASLGQKVTITCSASSSVSSLHWYQQKSGTSPKPWIYEISKLASGVPARFSG
                                                                                                                                                                                                                          2034; MHMS18.
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                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1JHL
                                                                                                                                                                                                                                       G195115; -.
                                                                                                                                                                                            V REGION;
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11502 MW;
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68
68
117
117
124
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                               FRAMEWORK 3.
D SEGMENT.
JH2 SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                       AS CLONED FROM A HYBRIDOMA MAKING (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 401; DB 1;
Pred. No. 1.2e-24;
                                                                                                                          IG HEAVY CHAIN V REGION (B1 FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
                                                                                              FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF938E49 CRC32
DEB2C7DA CRC32
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                                                                                                                                                                                                                                                                                                                                    Η.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    MAMMALIA;
                                                                                                                                                           (B1-8
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                                                                                                                                  Query Match
Best Local Similarity 78.1
Matches 82; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                          KAPPA CHAIN S107.
EMBL; J00577; G196764; --
EMBL; V00780; E1181574; --
PIR; A01943; KYMS7B.
HSSP; P01679; IFIG.
IMMUNOGLOBULIN V REGION; SIG
                                                                                                                                                                                   DISULFID
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SEQUENCE
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CHAIN
DOMAIN
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21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
1G KAPPA CHAIN PRECURSOR V-IV REGION (S107B).
MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 82115300.
KWAN S.-P., MAX E.E., SEIDMAN J.G., LEDER P.,
CELL 26:57-66(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KV4A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 YYWGQGTSVTVSS 239
||||||::||||
127 DYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
                                                                       61
                                                                                            26
                                                                                        THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE NORMAL
                                                  SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIK 105
                                                                                                                                                                                    129
129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                         129
45
57
72
711
111
118
128
                                                                                                                                                                                     13833 MW;
                                                                                                                                          31.1%;
78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.5%; Score 400; DB 1; Length 139; 58.6%; Pred. No. 1.9e-24;
                                                                                                                                                                                                                                                                                                           SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                  Score 395; DB 1; Length 129; Pred. No. 4.3e-24; 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                         IG KAPPA CHAIN V-IV REGION (S107B).
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                                                                                                                                                                                          ВY
                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING 3. FRAMEWORK 4.
                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3.
                                                                                                                                                                                   8D4D8311 CRC32;
                                                                                                                                                                                                       SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
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                                                                                                                                  4;
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 SPTREMBL_8:*

1: sp_fungd:
2: sp_invert
4: sp_manmal:
5: sp_inhc:*
6: sp_organe
7: sp_phage:
8: sp_organe
7: sp_bacter
10: sp_roden
11: sp_virus
12: sp_uncla
14: sp_uncla
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sp_organelle:*
sp_phage:*
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sp_bacteria:*
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sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_archea:*
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Copyright (c) 1993 - 1998 Compugen Ltd.
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sp_human:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4.5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
125.5	125.5	127	129.5	129.5	130	130.5	131.5	131.5	131.5	132	133	133.5	134	134	135
9.9	9.9	10.0	10.2	10.2	10.2	10.3	10.3	10.3	10.3	10.4	10.5	10.5	10.5	10.5	10.6
509	509	133	254	237	418	145	258	503	50	78	158	398	250	258	509
10	10	U1	12	12	10						12		12	12	10
035924	008907	Q31178	Q90557	Q90545	070426	Q16237	Q90559	P78324	Q15533	075720	Q90531	000241	Q90569	Q90556	P97710
mus	008907 mus musculu	Q31178 mus musculu	Q90557 ginglymosto	Q90545 ginglymosto	070426 rattus norv	Q16237 homo sapien	Q90559 ginglymosto	P78324 homo sapien	Q15533 homo sapien	075720 homo sapien	Q90531 ginglymosto	000241 homo sapien	Q90569 ginglymosto	Q90556 ginglymosto	P97710 rattus norv

# ALIGNMENTS

DE RA RA P	RES Q15 AC DT	2y 2	RP SQTTT SQTTT	RES OCC
AGMENT). S (HUMAN). WETAZOA; CHORDATA; VER HOMINIDAE; HOMO. OM N.A. CHIBANA K., TAKAYAMA N CHIBANA JO EMBL/GENB 1; G1262585;	RESULT 2 Q15535 ID Q15535 PRELIMINARY; PRT; 100 AA. AC Q15535; PRELIMINARY; PRT; 100 AA. DT 01-NOV-1996 (TREMBLREL 01, CREATED) DT 01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE) DT 01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)	3 LTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWYDTSKLASGVPGRE 60	SEQUENCE FROM N.A.  JANON K.; SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.  EMBL; X79906; E269393; ALT_TERM. IMMUNOCLOBULIN V REGION; SIGNAL. 22 POTENTIAL. SIGNAL 12 POTENTIAL. CHAIN 23 130 IG KAPPA CHAIN V REGION. SEQUENCE 130 AA; 14124 MW; 1DC6F7D9 CRC32; SEQUENCE 130 AA; 14124 MW; 1DC6F7D9 CRC32;  Query Match Best Local Similarity 79.0%; Pred. No. 9.6e-26; Best Local Similarity 79.0%; Pred. No. 9.6e-26; Matches 83; Conservative 8; Mismatches 12; Indels 2; Gaps	RESULT 1  PRO913  PRELIMINARY; PRT; 130 AA.  PRO913;  PRELIMINARY; PRT; 130 AA.  PRO913;  PRECIMINARY; PRT; 130 AA.  PRO913;  PRECIMINARY; PRT; 130 AA.  PRO913;  PRECIMINARY; PRT; 130 AA.  PRO913;  PRO913;  PRECIMINARY; PRECIMINARY; PRT SEQUENCE UPDATE;  PRO913;  PRO913; PRECIMINARY; PROPINARY; P

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Best Local :
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Best Local
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01-NOV-1998 (
01-NOV-1998 (
01-NOV-1998 (
IG HEAVY CHAI
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SEQUENCE
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
IG HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human IgA and IgM secreting intestinal plasma cells mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
FISCHER M.,
                      TISSUE-INTESTINE;
                                            SEQUENCE FROM N.A.
                                                                                     PRIMATES;
                                                                                                                                                                                                                                                                                       075741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ009521; E1311442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FISCHER M., KUEPPERS R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 YIHWYKORPEQGLEWIGWIHPENGNTYYDPKFQGKASITADTSSNAAYLQLSSLTSEDTA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                     211 VYYCA-----SYYYYSAYYAMYYW 229
                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YWTWIRQPPGKGLEWIGFIY-YSGNTNYNPSLKSRLTISVDTSKNQFSLKLTSMTAADTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGIHLP
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Y CHAIN VARIABLE I
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                                                                                       CATARRHINI;
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100 AA;
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                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                       HOMINIDAE;
                                                                                                                                                                   08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
REGION (FRAGMENT).
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REGION (FRAGMENT).
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Pred. No. 6e-08;
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Pred. No. 1.1e-09;
9; Mismatches 31
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01-NOV-1998 (TREMBLREL 08
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Best Local S
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075736;
01-NOV-1998
01-NOV-1998
01-NOV-1998
PRIMATES;
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"Human IgA and IgM secreting intestinal plasma
mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA
EMBL; AJ009534; E1311466; -..
NON_TER 1 1
NON_TER 8.1 8.1
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SUBMLITIED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009540; E1311476; -.

NON_TER 1 1
NON_TER 77 77
NON_TER 77 77
SEQUENCE 77 AA; 8734 MW; 1F7F9E8E CRC32;
                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                          210
                                                                                                                                                                                                                                                      152 IHWVKQRPEQGLEWIGWIHPENGN--TVYDPKFQGKASITADTSSNAAYLQLSSLTSEDT 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 CASYYYYSAYYAMYYW 229
                                                                                                                                                                                   63
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-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE |
-NOV-1998 (TREMBLREL. 08, LAST ANNOTATIO)
HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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                                                                                                                                                                                                AVYYCASY--YYYSAYYAMYYW
                                                                                                                                                                                   AVYYCVAYEGYY - - - YYGMDAW
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35; Conserv
                                                                                                                                                                                                                                                                              Similarity 45.1
37; Conservative
            CATARRHINI;
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9375 MW;
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            HOMINIDAE;
                                                          08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
REGION (FRAGMENT).
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Pred.
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Pred. No. 1.8e-07;
3; Mismatches 25;
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RESULT
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Immtated VH region genes.";
ISUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DA:
R EMBL; AJ009531; E1311462; -.
NON_TER 1 1
NON_TER 01
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Best Local Similarity
Matches 30; Conserv
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Best Local
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mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ
EMBL; AJ009523; E1311446; -.
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
IG HEAVY CHAIN VARIABLE
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TISSUE=INTESTINE;
FISCHER M., KUEPPE
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISCHER M., KUEPPERS R.;
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SAPIENS (HUMAN).
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42.58;
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
REGION (FRAGMENT).
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
REGION (FRAGMENT).
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Pred. No. 4.4e-07;
7; Mismatches 23
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Pred. No. 1.9e-07;
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PRIMATES; C
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NON_TER 1 1 1
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SEQUENCE 82 AA; 9566 MY
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SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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Pred. No. 4.7e-07;
4; Mismatches 22;
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8; Mismatches
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Pred. No. 6.
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mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ
EMBL; AJ009524; E1311148;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
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Pred. No. 6.5e-07;
5; Mismatches 24
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SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009537; E1311470; -...
NON_TER 1 1
NON_TER 72 72
SEQUENCE 72 AA; 8345 MW: FORDAAA
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SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA
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                                                                                                         152 IHWYKQRPEQGLEWIGWIHPENGN--TVYDPKFQGKASITADTSSNAAYLQLSSLTSEDT
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                                        210 AVYYCASYYYYSAYYAMYYW
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  AVYYCA--
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                                                                                                                                                                l Similarity
35; Conserv
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METAZOA; CHORDATA; VERTEBRATA;
CATARRHINI; HOMINIDAE; HOMO.
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METAZOA; CHORDATA;
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GREMBLREL.
GREMBLREL.
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E REGION (FRAGMENT).
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08, LAST ANNOTATION UPDATE)
REGION (FRAGMENT).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.8e
L2; Mismatches
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Pred. No. 9.9e
L6; Mismatches
                                                                                                                                                                                                                                                                       C95EB66A CRC32;
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                                                                                                                                                                                    DB 2;
.8e-06;
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RESULT

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RESULT 15
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Best Local Similarity
Matches 31; Conserv
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Best Local Similarity 40.5%;
Matches 32; Conservative 2
                                                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
SEQUENCE
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"Human 19A and 19M secreting intestinal plasma cells carry heavily mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009539; E1311474; -.
NON_TER 1 1
NON_TER 86 86
SEQUENCE 86 AA; 9625 MW; 07627E8C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             075740:
01-NOV-1998 (TREMBLREL. 08, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-INTESTINE;
FISCHER M., KUEPPERS R.;
"Human IgA and IgM secreting intestinal plasma cells carry heavily mutated VH region genes.";
SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ009538; E1311472; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01.NOV-1998 (TREMBLREL, 08, CREATED)
01.NOV-1998 (TREMBLREL, 08, LAST SEQUENCE UPDATE)
01.NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 YIHWVKORPEQGLEWIGWI--HPENGNTVYDPKFQGKASITADTSSNAAYLQLSSLISED 208
211 VYYCASYYYYSAYYAMYYW 229
                                                                                                        151 YIHWVKQRPEQGLEWIGWIHPENGNTVYDPKFQGKASITADTSSNAAYLQLSSLTSEDTA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 TAVYYCTT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 WMNWVRQAPGKGLEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTED 62
                                                                        1 YWSWIRQSPGKGLEWIGYIY-YTGSINYNPSLKSRVTISLGTSENQFSLNLTSVTAADTA 59
                                                                                                                                                                                                                                                                                                                               78 AA;
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                                                                                                                                                                                                                                                                                                                                  9031 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 167; DB 2; 1
Pred. No. 2.4e-06;
.5; Mismatches 20;
                                                                                                                                                                                       Score 166; DB 2; 1
Pred. No. 2.6e-06;
10; Mismatches 23;
                                                                                                                                                                                                                                                                                                                               05D273B9 CRC32;
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60 VYFCAR---HSSSWPIYYF 75

Search completed: May 13, 1999, 10:05:19 Job time: 657 sec

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Anti-human SC sing Fv(GP-4) immunosup

ALIGNMENTS

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein protein search, using sw model

Run on: May 13, 1999, 10:02:41; Search time 23.53 Seconds (without alignments) 206.293 Million cell updates/sec

Title: Perfect score: Sequence: US-08-704-178-4 1271 1 MQLTQSPAIMSASPGEKVTM.....SAYYAMYYWGQGTSVTVSSY 240

Scoring table:

BLOSUM62

Searched: 162890 seqs, 20225328 residues

Database : A\_Geneseq\_34:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.

Score

Query Match Length DB

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Description

1 1264 99. 3 829.5 65. 4 821.5 64. 4 821.5 64. 4 821.5 62. 6 795.5 62. 7 790.5 62. 7 790.5 59. 11 752.5 59. 11 772.5 57. 11 772.5 57. 12 772.5 57. 12 772.5 57. 13 772.5 57. 14 774.5 57. 15 772.5 57. 17 725.5 57. 18 725.5 57. 19 725.5 57. 20 725.5 57. 21 725.5 57. 22 725.5 57. 23 724 57. 24 57. 25 772.5 55. 36 771.5 56. 37 771.5 56. 38 770.5 55. 38 770.5 55. 39 700.5 55. 39 700.5 55. 40 698.5 55.	
4 239 1 W15186 238 1 R65783 3 244 1 R65783 6 237 1 W15186 6 237 1 W15185 2 236 1 R45443 7 240 1 W257483 7 240 1 W257483 7 240 1 W25783 9 239 1 W325783 9 239 1 R43679 9 239 1 R42679 1 473 1 W26646 473 1 W26648 1 473 1 W26648 1 51 1 W26648 1 1 W26648 1 1 W26688 1 1 W35128 1 W35128 1 W35128 1 W35128 1 W35128	
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	1 MQLTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWVYDTSKLASGVPGRF 60	1 MQLTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWVYDTSKLASGVPGRF 60	Query Match 99.4%; Score 1264; DB 1; Length 239; Best Local Similarity 100.0%; Pred. No. 4.5e-82; Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps (	Sequence 239 AA;	n coupled to a cytotoxic agent, to trea	ovarian and non-small cell lung of	diagnosis of tumour cells which overexpress the erbB-2 gpl85	Is userur	a sequence encoding a	coding for the heavy- and light- chain variable regions were then		by standard techniques. Messenger RNA coding for the anti-erbB-2	the gp185 protein, removing spleen cells and producing hybridomas	was generated by immunising mice with N/erbB-2 cells overexpressing	designated e21(Fv), which binds to erbB-2. Monoclonal antibody e21	The present sequence represents a claimed single-chain antibody,	Claim 2; Columns 27-30; 28pp; English.		=	Single chain antibodies specific for erbB-2 protein, gp185 - with	N-PSDB; T65007.	97-064831/06.	Bird RE, Kasprzyk PG, King CR;			30-JUN-1992; US-906555.			24-DEC-1996.	US5587458-A.	/labe	ion	Key Location/Qualifiers	Synthetic.	Mus musculus.	diagnosis; treatment; cytotoxic agent; e	cancer; ovarian cancer; non-small cell lung ca		5	05-JUN-1997 (first entry)	••	W15186 standard; Protein; 239 AA.	86	LT 1	
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RESULT
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Best Local Similarity
Matches 238; Conserv
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21-OCT-1992;
30-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 8; 37pp; English.

The source of human erbB-2 protein for the prodn. of antibodies no 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbB-2 protein on its surface (N/erbB-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbB-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. I animals given a combination of the 2 Abs, tumours completely regressed after 11 days.
                                                                                     (AJIN )
Hamura J
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R45443;
                                                                                                                       26-OCT-1994.
21-APR-1994; 106257.
21-APR-1993; JP-094491.
07-MAR-1994; JP-036065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of malignancies over 2 monoclonal antibodies which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR ONCOLOGY Kasprzyk PG, King CR; WPI; 94-025878/03.
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WO9400136-A.
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Sequence of the
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R60780;
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                                     N-PSDB; Q73678.
                                                       Takeshita
WPI; 94-31
                                                                                                                                                                                            EP-621338-A.
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                                                                                                                                                                                                                                                                            Fv(GP-2) immunosuppressive
   Immunosuppressant polypeptide
interleukin-2 response
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antibody variable region; GP-2; ]
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                                                     94-325948/41.
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                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                       AJINOMOTO
                                                                                       Kanayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AA;
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e single chai
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l antibody; cancer therapy; preventio
                                                                                        Nakazawa
                                                                                                                                                                                                                                                                                                                                244
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nich recognise different e
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Pred. No. 1e-81;
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                   ability
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                                                                                   Sugamura
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N-PSDB;
                 Rapid
by fus
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 fusing genes with rget cells
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28-MAY-1991.
11-JAN-1990;
11-JAN-1990;
(USSH) NAT I
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OVB3 light and heavy chains.
Immunoglobulin; immunotoxin;
pseudomonas exotoxin.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 26-27; 37pp; English.

MAB capable of binding to the gamma chain of the IL-2 recept
thus of blocking the IL-2 response, is produced by mouse byt
line GP-2 (FERM BP-4641). DNA encoding the variable region
this MAB was expressed in E. coli, yielding Fv(GP-2) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R12798 standard;
R12798;
in 1;
91-200877/27.
91-200877/27.
DB; Q12405.
d cloning of antibody genes as single chain immuno-toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTQSPAIMSASPGEKYTMTCSASSSVSN--MHWYQQKSSTSPKLWVYDTSKLASGVPGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKFKSKATLTVDTSSSTAYMHLSSLTSEDSAVYYCTRSSRNWVYYAMDYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIK-GSTSGSGKSSEGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQLQQSGYELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTQSPSIMSASLGERVTMTCTASSSVSSSYLHWYQQKPGSSPKLWIYSTSNLASGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKLEESGSELVRPGASVKLSCKASGYTFTSYWMHWVKQRHGQGLEWIGNIYPGSGSTNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunotoxin; antibody;
                                                                                                                  ç
                                                                                                                                                                                                                /label=
121. .13
                                                                                                                                                                                                                                                           219. .229
/label- CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                          170. .186
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- Light chain
108. .121
                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                        labe
                                                                                                                                                                                                                                                                                                                                                                                                                      label- CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= Heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                             labe.
                                                                                                                                                                                                                                                                                                                                                           label-
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                                                                                                                  HEALTH
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68.3%;
                                                                                                                                                                                                                                                                                                                            .155
L- CDR1
                                                                                                                                                                                                                                                                                                                                                             · CDR3
                                                                                                                                                                                                                                                                                                                                                                                           CDR2
                                                                                                                                                                                                 N-terminal
                                                                                                                                                                                                                                N-terminal
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RESULP RE
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                                                                                                                                                                                      inhibition of proliferation or survival of, esp. malignant erbB2, realls - by introducing nucleic acid mol. encoding antibody homologue which is expressed and binds, pref. erbB2, protein intracellularly bisclosure; page 29-30; 48pp; English.

A nucleic acid comprises a first sequence encoding a signal peptide (R94019) linked to a second sequence (T17728) encoding a single chain Fv fragment (R94020) that binds a human erbB2 oncoprotein.

The anti-erbB2 sFv portion is obtained by PCR using e23scFv plasmid as template. The signal peptide directs the scFv to the endoplasmic reticulum. The nucleic acid is incorporated into a plasmid or viral vector to facilitate expression of the scFv antibody homologue within e.g. an epithelial carcinoma cell. Intracellular expression of the homologue inhibits surface expression of erbB2 and thereby inhibits cell proliferation and cell survival and decreases
  Query Match
Best Local Sin
Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-1996.
23-AUG-1995; U10740.
06-SEP-1994; US-301339.
06-JUN-1995; US-468252.
(UABR-) UAB RES FOUND.
CUTIEL DT, Deshane J;
WPI; 96-171307/17.
N-PSDB; T17728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy.
Synthetic.
                                                                                                                                                tumorigenicity.
Sequence 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R94020 standard; Protein;
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQQSGVELVRGGALVKLSCKASDENIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -FQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWGGGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVESGGGLVQPGGSRQLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYI-SRGGNTIYYAN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVKGRFTISRDNPKNTLFLQMTSLRSDDTAMYYCARSHYYGYFYAMDYWGQGTTLTGSS
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     Conservative
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                               62.6%;
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     32;
                               Score 795.5; DB Pred. No. 3.3e-49
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Pred. No. 5.1e-51;
1; Mismatches 47
     Mismatches
5; DB 1;
3.3e-49;
nes 45;
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MQLTQSPAIMSASPGEKVTMTCSASSSVSNMHWYQQKSSTSPKLWVYDTSKLASGVPGRF

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61

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Matches

155;

Conservative

32;

Indels

9

Gaps

2

60

62

Similarity

LQLTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPARF

SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV

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cells expressing this process. Staim 2: Columns 25-28; 28pp; English.

Claim 2: Columns 25-28; 28pp; English.

Chaim 2: Columns 25-28; 25pp; English.

Chaim 2: Columns 2: Column
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Best Local
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07-OCT-1991; 772270.
07-OCT-1991; US-772270.
07-OCT-1991; US-906555.
30-JUN-1992; US-906555.
14-MAY-1993; US-061092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single chain antibodies specific for erbB-2 protein, gp185 labels or cytotoxin, useful for detection and treatment of cells expressing this protein cells expressing this protein claim 2; Columns 25-28; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bird RE, Kasprzyk PG, King WPI; 97-064831/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single chain antibody; variable region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCA---SYYYYSAYYAMYYWGQGTSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLQESGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEGKGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-erbB2 antibody e23(Fv).
antibody; variable region; light chain; heavy chain;
r; ovarian cancer; non-small cell lung carcinoma;
sis; treatment; cytotoxic agent; erbB-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 108. .121
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                          62.6%;
Score 795.5;
Pred. No. 3.3e
32; Mismatches
                          5; DB 1;
3.3e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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Best Local S
Matches 154
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06-CAN-1992; U08545.

30-JUN-1992; US-906555.

(MOLE-) MOLECULAR ONCOLOGY II

Kasprzyk PG, King CR;

WPI; 94-025878/03.
                                                                                                                                                                                                                                                                The source of human erbb-2 protein for the prodn. of antibodies n 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell 23 and 21 (Q55180/R45442; Q55181/R45443) is a NIH/3T3 cell engineered to express the human erbb-2 protein on its surface (N/erbb-2). Abs no. 21 and 23 are directed against the extracellular domain of gp185 erbb-2. Nude mice manipulated to produce rapidly growing tumours were used in a trial of the efficacy of the Abs. animals given a combination of the 2 Abs, tumours completely regressed after 11 days.
                                                                                                                                                                                                                                                                                                                                                             gp185
                                                                                                                                                                                                                                                                                                                                                                                                                                                        monoclonal antibody.
Synthetic.
WO9400136-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1994 (first entry)
Sequence of the single chain anti-
Single chain anti-erbBl antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R45442;
21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                        2 monoclonal
                                                                                                                                                                                                                                                                                                                                                                               Treatment of malignancies
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q55180
                                                                                                                                                                                                                                                                                                                                                     Example; Fig 7;
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                                                                                                                                                   SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV
                                                                 KFKGKATFTV
                                                                                 KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCA---SYYYYSAYYAMYYWGQGTSVTV
                                                                                                    QLQDSGPEVVKPGGSMKISCKTSGYSFTGHTMNWVKQSHGKNLEWIGLINPYNGDTNYNQ
                                                                                                                                         SGGGSGTSYSLTVSRVEAEDAATYYCQQWSRSPPTFGGGSKLEIKGSTSGSGKSSEGKGV
                                                                                                                                                                                LQLTQSPAILSASPGEKVTMTCRATPSVSYMHWYQQKPGSSPKPWIYTTSNLASGVPARF
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                                                                                                                                                                                                                            62.2%;
                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                       which
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                                                                                                                                                                                                                                                                                                                                                                      over-expressing ERB-[2 - using at hich recognise different epitopes of
                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                   Score 790.5;
Pred. No. 7.5e
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-erbB2 antibody,
body; cancer therapy;
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                                                                                                                                                                                                                             .5e-49;
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                                                                                                                                                                                                                                    Length
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                                                                 WGAGTTVTV
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Best Local S
Matches 149
                                                      WPI; 97-
N-PSDB;
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R15443;
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RESULT

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cell(
ce fv fragment encoded by pSCVI was able to proceed infection by HRV-14. It was less active than mod ce which included a Gly-Gly-Gly-Gly-Ser flexible lift ce and H chains as either a monomer or a dimer see also R15437-R15442.

Sequence 240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen-binding fragment; inflamm Homo sapiens.

EP-459577-A.
04-DEC-1991.
04-DEC-1991.
25-MAY-1991; 201243.
01-JUN-1990; US-532001.
(MERI ) MERCK & CO INC.
(Colonno RJ, Condra JH, Tomassini WPI; 91-35580/49.
Microbially expressed portions of attachment of rhinovirus ligands
                                                                                                                                                                                                                                                                                                   Anti-spl30 (first entry)
Anti-spl30 antibody derived scFv.
Single chain Fv; scFv; antibody; E. coli; anti-T3 antibody; anti-gpl30 antibody; inclusion body; chaperonin.
Synthetic.
Synthetic.
J09220092-A.
26-AUG-1007
Producing single chain Fv antibody in Escherichia coli - by expression in an inclusion body, followed by protein folding co-expression with a chaperonin as a soluble fraction Claim 4; Page 6-7; 9pp; Japanese.

The sequences given in W25783-84 represent single chain Fv (antibodies which are produced in E.coli. The scFV's are derivant to the scFV's are derivative for the scFV's are derivative fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1992
Single chain
                                                                                                                                                        (TOYJ ) TOSOH CORP.
WPI; 97-474306/44.
N-PSDB; T91615.
                                                                                                                                                                                                                                           15-FEB-1996; 027622.
15-FEB-1996; JP-027622.
                                                                                                                                                                                                                                                                                                26-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGVQLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTV 177
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Pred. No. 6.5e
33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single chain anti-Fc gamma RI antibody fused to anti-CEA Humanised antibody; anti-Fc receptor; H22; bifunctional; fusion protein; chimera; carcinoembryonic antigen; CEA.
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Pred. No. 1.2e
31; Mismatches
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07-JUN-1995; US-484172.
(MEDA-) MEDAREX INC.
Deo YM, Goldstein J, Graz
WPI; 99-023374/02.
N-PSDB; V08176.
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07-JUN-1995; US-484172.
(MEDA-) MEDAREX INC.
Deo YM, Goldstein J, G
                                                                                                                                                                                                                                                                             25-JAN-1999 (first entry)

122-anti-CEA antibody construct 321.

123-Multispecific single chain antibody; antibody H22; tumour cell; therapy; antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection; epidermal growth factor receptor; breast cancer; ovarian cancer.

125-JAN-1999 (first entry)

126-JAN-1999 (first entry)
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07-JUN-1996;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    also comprise an anti-target portion, used for the treatment of cancer, autoimmune disease and pathogenic infection Example 8; Fig 40; 115pp; English.

A mammalian expression construct encoding a single chain antibody having binding specificity for Fc gamma RI, derived from the humanised anti-Fc gamma RI monoclonal antibody H22 was prepared (see T58129). A bispecific single chain polypeptide was produced by fusing the H22 scFv to an anti-carcinoembryonic antigen (CEA) antibody. The H22-anti-CEA fusion protein was shown to bind both for gamma RI and CEA.
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Sequence
specific killing of tumour cells - using comprising an anti-Fc receptor antibody a
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                        Specific killing of tumour cells -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVPGRFSGSGSGNSYSLTISSMEAEDAATTYCYQGSGY--PFTFGSGTKLEIKGSTSGS 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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"6 histidine residues"
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Pred. No. 9.4e-46;
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and a portion which binds
                        a multi-specific molecule
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RESULT
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Example 8; Fig 40; 57pp; English.

CC This sequence represents the construct 321, which is a fusion between an CC anti-CEA antibody and a multispecific single chain antibody designated CC 422. The antibody can be used in the method of the invention for inducing CC antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell CC which is characterised by overexpression of HER 2/neu or epidermal growth CC factor receptor (EGFR), comprises contacting the tumour cell with a CC multispecific protein molecule (preferably a single chain antibody) CC comprising: (a) an anti-FC receptor antibody or an antigen bhinding CC fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which binds to EGFR. The method can be used for treating cancers especially CC breast cancer or ovarian cancer. The multispecific antibody can also be administered prophylactically to vaccinate a subject against infection CC by a target cell.
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Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                       21-MAY-1996.
02-SEP-1986; US-902971.
02-SEP-1986; US-902971.
02-SEP-1987; US-902110.
19-JAN-1989; US-299617.
25-APR-1990; US-513910.
01-APR-1993; US-40404.0
06-JUN-1995; US-468988.
(ENZO-) ENZON LABS INC.
Immunoassay using single chain antigen binding for labelled or immobilised antibody, are less to engineer, more stable and less expensive Example 9; Fig 39A-B; 78pp; English.

Computer-designed construct 18-2-3/TRY202' (W02 the DNA sequence given in T36463, comprises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody engineering; monoclonal antibody; MAb; single chain antibody; immunoassay; fluorescein single chain binding protein.
                                                                                                                                                                                                    Bird RE, Hardman K, Ladner RC; wPI; 96-259060/26.
                                                                                                                                                                            N-PSDB; T36463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5518889-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric synthetic.
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18-2-3/TRY202' single chain binding protein.
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Pred. No. 9.
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.4e-46;
  (W02191), encoded by the variable regions
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                                                                                              N. PSDB; Q51340.**

N. PSDB; Q51340.**

Single chain poly:peptide for binding antigen - comprising light and heavy chain antigen binding portions linked by peptide linker Example 9; Figure 39; 78pp; English.

The single chain polypeptide is derived from the mature light and the single chain polypeptide is derived from the affinity for a given antigen (Fluorescell). It comprises a first polypeptide comprising the antigen binding portion of of the light chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the heavy chain variable region of an antibody and a second polypeptide region of an antibody and a second polypeptide cregion of an antibody and at least one peptide linker linking the first and second polypeptide chains. The resulting single chain collippeptide can be used in diagnostics, therapy collippeptide chain vitro and in vitro), imaging, purifications and biosensors. This particular single chain binding molecule was designated in 2-2-3/TRY202' and contains one linker peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 148
Query Match
Best Local Similarity
Matches 148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1993.

02-SEP-1986; 902971.

02-SEP-1986; US-902971.

02-SEP-1987; US-092110.

19-JAN-1989; US-299617.

25-APR-1990; US-512910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R43679 standard;
R43679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the light and heavy chains of anti-fluorescein monoclonal antibody (Mab) 18-2-3 linked by a peptide designed to fit into a groove on the backside of the variable domain structure. The DNA construct was inserted into vector pGX3703 and introduced into E. coli. 18-2-3/TRY202' was produced as a single chain molecule. It exhibited biological binding activity equivalent in specifically and affinity to that of the original Mab.
                                                                                                                                                                                                                                                                                                                                                                                            (ENZO-) ENZON INC.
Bird RE, Hardman K,
WPI: 93-367875/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single chain polypeptide with affinity for fluorescein. Monoclonal antibody; MAD; affinity; binding; antigen; diagnostics; therapy; imaging; purification; biosensors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALMSRLSISKDNSKSQVFLKMNSLQNDDTAIYYCAKRLGRIFYYAMDYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWGQGTSVTVS : ||: | | : :||:::|| :|||| |||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG--SESKST 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
148; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                58.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                Ladner
              Score 748.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 751.5; DB 1;
Pred. No. 4.1e-46;
0; Mismatches 55;
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            .7e-46;
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                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                   Immuno:purifien. using single binding chain molecule including antigen-binding parts of antibody light and heavy chain variable regions connected by a linker - is smaller, stabler and less respensive than complete antibodies

Example 9; Fig 39; 78pp; English.

A DNA construct (T13739) codes for single chain binding molecule R2-3/TRY202' (R99649), in which VL and VH regions of antifluorescein monoclonal antibody 18-2-3 are joined by a peptide linker composed primarily of alternating Gly and Ser residues, with Glu and Lys residues to enhance solubility. The construct was expressed in E.coli. Soluble, folded chain antibody (SCA) was cobtd. which was capable of exhibiting a biological binding activity equivalent in specificity and affinity to that of a monoclonal advantages of smaller size, greater stability and reduced cost.
                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1996.
02-SEP-1986;
02-SEP-1986;
02-SEP-1987;
19-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird RE, Hardman K,
WPI; 96-333309/33.
N-PSDB; T13739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-1990;
01-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single chain binding molecule 18-2-3/TRY202'.
Antibody engineering; single polypeptide chain binding single chain antibody; SCA; heavy chain; light chain; monocional antibody; MAb; immunoaffinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5534621-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R99649 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
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                                                                                                                                                                                           LTQSPAIMSASPGEKVTMTCSASSSVSN--MHWYQQKSSTSPKLWVYDTSKLASGVPGRF 60
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                                                                                 SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV 120
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  QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDP
                                                  SGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG--SESKST
                                                                                                                                                          LTQSPAIMSASPGEKVTMTCRASSSVSSSYLHWYQQKSGASPKLWVYGTSNLASGVPARF
                                                                                                                                                                                                                                                                          al Similarity
148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     of smaller size,
239 AA;
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US-902971.
US-092110.
US-299617.
US-512910.
US-512910.
US-468992.
                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                             Score 748.5; DB 1
Pred. No. 6.7e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
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                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                      Length
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Best Local
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US4946778-A.
07-AUG-1990.
19-JAN-1989; 299617.
02-SEP-1986; US-902971.
02-SEP-1987; US-092110.
19-JAN-1989; US-299617.
                                                                                                                                                                                                                                                                                       The sequence was constructed from the variable regions of an antifluorescein MAb, 18-3-2, an IgM. The VL and VH cDNA sequences were synthesised by priming on RNA isolated from hybridona cells. The sequence encodes a single chain binding molecule comprising the variable regions of heavy and light chains linked by peptides. The peptide linker was computer-designed to fit inyo a groove on the backside of the variable domain structure and is composed primarly of alternating Gly and Ser residues. Glu and Lys residues see also R06476-R06484.
                                                                                                                                                                                                                                                                                                                                                                                                                                              variable region.
Disclosure; Fig 39; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single polypeptide chain binding molecules - having light chavariable region of antibody linked by peptide to heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R06482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JAN-1991 (:
18-2-3-/TRY202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R06482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R06482 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
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  182
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                                                                                                                                                                                3 LTQSPAIMSASPGEKVTMTCSASSSVSN--MHWYQQKSSTSPKLWVYDTSKLASGVPGRF
               QLQQSGVELVRGGALVKLSCKASDFNIKDYYIHWVKQRPEQGLEWIGWIHPENGNTVYDP 180
                                                                                                                         SGSGSGNSYSLTISSMEAEDAATYYCYQGSGYPFTFGSGTKLEIKGSTSGSGKSSEGKGV 120
                                                                                                                                                                 LTQSPAIMSASPGEKVNMTCRASSSVSSSYLHWYQQKSGASPKLWVYGTSNLASGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  er RC, Bird RE, Hardman 90-260350/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALMSRLSISKDNSKSQVFLKMNSLQIDDTAIYYCAKRLGRIFYYAMDYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFQGKASITADTSSNAAYLQLSSLTSEDTAVYYCASYYYYSAYYAMYYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147;
ALMSRLSISKDNSKSQVFLKMNSLQIDDTAIYYCAKRLERIFYYAMDYWGQGTSVTVS
                                                                                                            SGGGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELEGKSSGSG--SESKST 122
                                                      QLKESGPVLVAPSQSLSITCTVSGFSLTNYGVHWVRQPPGKGLEWLGVIW-AGGNTNYNS 181
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variable chain; anti-fluorescein
                                                                                                                                                                                                                                     58.6%;
61.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                     Score 744.5; DB 1;
Pred. No. 1.3e-45;
19; Mismatches 57;
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